

WHAT IS CLAIMED IS:

1. An isolated or recombinant nucleic acid comprising a nucleic acid
5 sequence having at least 50% sequence identity to SEQ ID NO:1, SEQ ID NO:3, SEQ ID
NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ
ID NO:17, SEQ ID NO:19, SEQ ID NO:21, SEQ ID NO:23, SEQ ID NO:25, SEQ ID NO:27,
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NO:39, SEQ ID NO:41, SEQ ID NO:43, SEQ ID NO:45, SEQ ID NO:47, SEQ ID NO:49,
10 SEQ ID NO:51, SEQ ID NO:53, SEQ ID NO:55, SEQ ID NO:57, SEQ ID NO:59, SEQ ID
NO:61, SEQ ID NO:63, SEQ ID NO:65, SEQ ID NO:67, SEQ ID NO:69, SEQ ID NO:71,
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NO:115, SEQ ID NO:117, SEQ ID NO:119, SEQ ID NO:121, SEQ ID NO:123, SEQ ID
NO:125, SEQ ID NO:127, SEQ ID NO:129, SEQ ID NO:131, SEQ ID NO:133, SEQ ID
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NO:245, SEQ ID NO:247, SEQ ID NO:249, SEQ ID NO:251, SEQ ID NO:253, SEQ ID
30 NO:255, SEQ ID NO:257, SEQ ID NO:259, SEQ ID NO:261, SEQ ID NO:263, SEQ ID
NO:265, SEQ ID NO:267, SEQ ID NO:269, SEQ ID NO:271, SEQ ID NO:273, SEQ ID
NO:275, SEQ ID NO:277, SEQ ID NO:279, SEQ ID NO:281, SEQ ID NO:283, SEQ ID
NO:285, SEQ ID NO:287, SEQ ID NO:289, SEQ ID NO:291, SEQ ID NO:293, SEQ ID
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NO:305, SEQ ID NO:307, SEQ ID NO:309, SEQ ID NO:311, SEQ ID NO:313, SEQ ID NO:315, SEQ ID NO:317, SEQ ID NO:319, SEQ ID NO:321, SEQ ID NO:323, SEQ ID NO:325, SEQ ID NO:327, SEQ ID NO:329, SEQ ID NO:331, SEQ ID NO:333, SEQ ID NO:335, SEQ ID NO:337, SEQ ID NO:339, SEQ ID NO:341, SEQ ID NO:343, SEQ ID NO:345, SEQ ID NO:347, SEQ ID NO:349, SEQ ID NO:351, SEQ ID NO:353, SEQ ID NO:355, SEQ ID NO:357, SEQ ID NO:359, SEQ ID NO:361, SEQ ID NO:363, SEQ ID NO:365, SEQ ID NO:367, SEQ ID NO:369, SEQ ID NO:371, SEQ ID NO:373, SEQ ID NO:375, SEQ ID NO:377 or SEQ ID NO:379, over a region of at least about 100 residues, wherein the nucleic acid encodes at least one polypeptide having a xylanase activity, and the sequence identities are determined by analysis with a sequence comparison algorithm or by a visual inspection.

2. The isolated or recombinant nucleic acid of claim 1, wherein the sequence identity is at least about 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, 60%, 61%, 62%, 63% or 64%.

3. The isolated or recombinant nucleic acid of claim 1, wherein the sequence identity is at least about 65%, 66%, 67%, 68%, 69%, 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or more sequence identity to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, SEQ ID NO:23, SEQ ID NO:25, SEQ ID NO:27, SEQ ID NO:29, SEQ ID NO:31, SEQ ID NO:33, SEQ ID NO:35, SEQ ID NO:37, SEQ ID NO:39, SEQ ID NO:41, SEQ ID NO:43, SEQ ID NO:45, SEQ ID NO:47, SEQ ID NO:49, SEQ ID NO:51, SEQ ID NO:53, SEQ ID NO:55, SEQ ID NO:57, SEQ ID NO:59, SEQ ID NO:61, SEQ ID NO:63, SEQ ID NO:65, SEQ ID NO:67, SEQ ID NO:69, SEQ ID NO:71, SEQ ID NO:73, SEQ ID NO:75, SEQ ID NO:77, SEQ ID NO:79, SEQ ID NO:81, SEQ ID NO:83, SEQ ID NO:85, SEQ ID NO:87, SEQ ID NO:89, SEQ ID NO:91, SEQ ID NO:93, SEQ ID NO:95, SEQ ID NO:97, SEQ ID NO:99, SEQ ID NO:101, SEQ ID NO:103, SEQ ID NO:105, SEQ ID NO:107, SEQ ID NO:109, SEQ ID NO:111, SEQ ID NO:113, SEQ ID NO:115, SEQ ID NO:117, SEQ ID NO:119, SEQ ID NO:121, SEQ ID NO:123, SEQ ID NO:125, SEQ ID NO:127, SEQ ID NO:129, SEQ ID NO:131, SEQ ID NO:133, SEQ ID NO:135, SEQ ID NO:137, SEQ ID NO:139, SEQ ID NO:141, SEQ ID NO:143, SEQ ID NO:145, SEQ ID NO:147, SEQ ID NO:149, SEQ ID

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 NO:361, SEQ ID NO:363, SEQ ID NO:365, SEQ ID NO:367, SEQ ID NO:369, SEQ ID
 NO:371, SEQ ID NO:373, SEQ ID NO:375, SEQ ID NO:377 or SEQ ID NO:379.

25 4. The isolated or recombinant nucleic acid of claim 1, wherein the
 sequence identity is over a region of at least about 50, 75, 100, 150, 200, 250, 300, 350, 400,
 450, 500, 550, 600, 650, 700, 750, 800, 850, 900, 950, 1000, 1050, 1100, 1150 or more
 residues, or the full length of a gene or a transcript.

30 5. The isolated or recombinant nucleic acid of claim 1, wherein the
 nucleic acid sequence comprises a sequence as set forth in SEQ ID NO:1, SEQ ID NO:3,
 SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID
 NO:15, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, SEQ ID NO:23, SEQ ID NO:25,
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NO:37, SEQ ID NO:39, SEQ ID NO:41, SEQ ID NO:43, SEQ ID NO:45, SEQ ID NO:47,
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5 NO:81, SEQ ID NO:83, SEQ ID NO:85, SEQ ID NO:87, SEQ ID NO:89, SEQ ID NO:91,
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NO:363, SEQ ID NO:365, SEQ ID NO:367, SEQ ID NO:369, SEQ ID NO:371, SEQ ID
NO:373, SEQ ID NO:375, SEQ ID NO:377 or SEQ ID NO:379.

6. The isolated or recombinant nucleic acid of claim 1, wherein the nucleic acid sequence encodes a polypeptide having a sequence as set forth in SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:12, SEQ ID NO:14, SEQ ID NO:16, SEQ ID NO:18, SEQ ID NO:20, SEQ ID NO:22, SEQ ID NO:24, SEQ ID NO:26, SEQ ID NO:28, SEQ ID NO:30, SEQ ID NO:32, SEQ ID NO:34, SEQ ID NO:36, SEQ ID NO:38, SEQ ID NO:40, SEQ ID NO:42, SEQ ID NO:44, SEQ ID NO:46, SEQ ID NO:48, SEQ ID NO:50, SEQ ID NO:52, SEQ ID NO:54, SEQ ID NO:56, SEQ ID NO:58, SEQ ID NO:60, SEQ ID NO:62, SEQ ID NO:64, SEQ ID NO:66, SEQ ID NO:68, SEQ ID NO:70, SEQ ID NO:72, SEQ ID NO:74, SEQ ID NO:76, SEQ ID NO:78, SEQ ID NO:80, SEQ ID NO:82, SEQ ID NO:84, SEQ ID NO:86, SEQ ID NO:88, SEQ ID NO:90, SEQ ID NO:92, SEQ ID NO:94, SEQ ID NO:96, SEQ ID NO:98, SEQ ID NO:100, SEQ ID NO:102, SEQ ID NO:104, SEQ ID NO:106, SEQ ID NO:108, SEQ ID NO:110, SEQ ID NO:112, SEQ ID NO:114, SEQ ID NO:116, SEQ ID NO:118, SEQ ID NO:120, SEQ ID NO:122, SEQ ID NO:124, SEQ ID NO:126, SEQ ID NO:128, SEQ ID NO:130, SEQ ID NO:132, SEQ ID NO:134, SEQ ID NO:136, SEQ ID NO:138, SEQ ID NO:140, SEQ ID NO:142, SEQ ID NO:144, SEQ ID NO:146, SEQ ID NO:148, SEQ ID NO:150, SEQ ID NO:152, SEQ ID NO:154, SEQ ID NO:156, SEQ ID NO:158, SEQ ID NO:160, SEQ ID NO:162, SEQ ID NO:164, SEQ ID NO:166, SEQ ID NO:168, SEQ ID NO:170, SEQ ID NO:172, SEQ ID NO:174, SEQ ID NO:176, SEQ ID NO:178, SEQ ID NO:180, SEQ ID NO:182, SEQ ID NO:184, SEQ ID NO:186, SEQ ID NO:188, SEQ ID NO:190, SEQ ID NO:192, SEQ ID NO:194, SEQ ID NO:196, SEQ ID NO:198, SEQ ID NO:200, SEQ ID NO:202, SEQ ID NO:204, SEQ ID NO:206, SEQ ID NO:208, SEQ ID NO:210, SEQ ID NO:212, SEQ ID NO:214, SEQ ID NO:216, SEQ ID NO:218, SEQ ID NO:220, SEQ ID NO:222, SEQ ID NO:224, SEQ ID NO:226, SEQ ID NO:228, SEQ ID NO:230, SEQ ID NO:232, SEQ ID NO:234, SEQ ID NO:236, SEQ ID NO:238, SEQ ID NO:240, SEQ ID NO:242, SEQ ID NO:244, SEQ ID NO:246, SEQ ID NO:248, SEQ ID NO:250, SEQ ID NO:252, SEQ ID NO:254, SEQ ID NO:256, SEQ ID NO:258, SEQ ID NO:260, SEQ ID NO:262, SEQ ID NO:264, SEQ ID NO:266, SEQ ID NO:268, SEQ ID NO:270, SEQ ID NO:272, SEQ ID NO:274, SEQ ID NO:276, SEQ ID NO:278, SEQ ID NO:280, SEQ ID NO:282, SEQ ID NO:284, SEQ ID NO:286, SEQ ID NO:288, SEQ ID NO:290, SEQ ID NO:292, SEQ ID NO:294, SEQ ID NO:296, SEQ ID NO:298, SEQ ID NO:300, SEQ ID NO:302, SEQ ID NO:304, SEQ ID NO:306, SEQ ID NO:308, SEQ ID NO:310, SEQ ID NO:312, SEQ ID NO:314, SEQ ID NO:316, SEQ ID NO:318, SEQ ID NO:320, SEQ ID NO:322,

SEQ ID NO:324, SEQ ID NO:326, SEQ ID NO:328, SEQ ID NO:330, SEQ ID NO:332,
SEQ ID NO:334, SEQ ID NO:336, SEQ ID NO:338, SEQ ID NO:340, SEQ ID NO:342,
SEQ ID NO:344, SEQ ID NO:346, SEQ ID NO:348, SEQ ID NO:350, SEQ ID NO:352,
SEQ ID NO:354, SEQ ID NO:356, SEQ ID NO:358, SEQ ID NO:360, SEQ ID NO:362,
5 SEQ ID NO:364, SEQ ID NO:366, SEQ ID NO:368, SEQ ID NO:370, SEQ ID NO:372,
SEQ ID NO:374, SEQ ID NO:376, SEQ ID NO:378 or SEQ ID NO:380.

7. The isolated or recombinant nucleic acid of claim 1, wherein the
sequence comparison algorithm is a BLAST version 2.2.2 algorithm where a filtering setting
10 is set to blastall -p blastp -d "nr pataa" -F F, and all other options are set to default.

8. The isolated or recombinant nucleic acid of claim 1, wherein the
xylanase activity comprises catalyzing hydrolysis of internal β -1,4-xylosidic linkages.

15 9. The isolated or recombinant nucleic acid of claim 8, wherein the
xylanase activity comprises an endo-1,4-beta-xylanase activity.

10. The isolated or recombinant nucleic acid of claim 1, wherein the
xylanase activity comprises hydrolyzing a xylan to produce a smaller molecular weight
20 xylose and xylo-oligomer.

11. The isolated or recombinant nucleic acid of claim 10, wherein the
xylan comprises an arabinoxylan.

25 12. The isolated or recombinant nucleic acid of claim 11, wherein the
arabinoxylan comprises a water soluble arabinoxylan.

13. The isolated or recombinant nucleic acid of claim 12, wherein the
water soluble arabinoxylan comprises a dough or a bread product.

30 14. The isolated or recombinant nucleic acid of claim 1, wherein the
xylanase activity comprises hydrolyzing polysaccharides comprising 1,4- β -glycoside-linked
D-xylopyranoses.

15. The isolated or recombinant nucleic acid of claim 1, wherein the xylanase activity comprises hydrolyzing hemicelluloses.

16. The isolated or recombinant nucleic acid of claim 15, wherein the xylanase activity comprises hydrolyzing hemicelluloses in a wood or paper pulp or a paper product.

17. The isolated or recombinant nucleic acid of claim 8, wherein the xylanase activity comprises catalyzing hydrolysis of xylans in a feed or a food product.

18. The isolated or recombinant nucleic acid of claim 17, wherein the feed or food product comprises a cereal-based animal feed, a wort or a beer, a milk or a milk product, a fruit or a vegetable.

19. The isolated or recombinant nucleic acid of claim 1, wherein the xylanase activity comprises catalyzing hydrolysis of xylans in a microbial cell or a plant cell.

20. The isolated or recombinant nucleic acid of claim 1, wherein the xylanase activity is thermostable.

21. The isolated or recombinant nucleic acid of claim 20, wherein the polypeptide retains a xylanase activity under conditions comprising a temperature range of between about 37°C to about 95°C, or between about 55°C to about 85°C, or between about 70°C to about 75°C, or between about 70°C to about 95°C, or between about 90°C to about 95°C.

22. The isolated or recombinant nucleic acid of claim 1, wherein the xylanase activity is thermotolerant.

23. The isolated or recombinant nucleic acid of claim 22, wherein the polypeptide retains a xylanase activity after exposure to a temperature in the range from greater than 37°C to about 95°C, from greater than 55°C to about 85°C, or between about 70°C to about 75°C, or from greater than 90°C to about 95°C.

24. An isolated or recombinant nucleic acid, wherein the nucleic acid comprises a sequence that hybridizes under stringent conditions to a nucleic acid comprising SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, SEQ ID
5 NO:23, SEQ ID NO:25, SEQ ID NO:27, SEQ ID NO:29, SEQ ID NO:31, SEQ ID NO:33, SEQ ID NO:35, SEQ ID NO:37, SEQ ID NO:39, SEQ ID NO:41, SEQ ID NO:43, SEQ ID NO:45, SEQ ID NO:47, SEQ ID NO:49, SEQ ID NO:51, SEQ ID NO:53, SEQ ID NO:55, SEQ ID NO:57, SEQ ID NO:59, SEQ ID NO:61, SEQ ID NO:63, SEQ ID NO:65, SEQ ID NO:67, SEQ ID NO:69, SEQ ID NO:71, SEQ ID NO:73, SEQ ID NO:75, SEQ ID NO:77,
10 SEQ ID NO:79, SEQ ID NO:81, SEQ ID NO:83, SEQ ID NO:85, SEQ ID NO:87, SEQ ID NO:89, SEQ ID NO:91, SEQ ID NO:93, SEQ ID NO:95, SEQ ID NO:97, SEQ ID NO:99, SEQ ID NO:101, SEQ ID NO:103, SEQ ID NO:105, SEQ ID NO:107, SEQ ID NO:109, SEQ ID NO:111, SEQ ID NO:113, SEQ ID NO:115, SEQ ID NO:117, SEQ ID NO:119, SEQ ID NO:121, SEQ ID NO:123, SEQ ID NO:125, SEQ ID NO:127, SEQ ID NO:129,
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20 SEQ ID NO:181, SEQ ID NO:183, SEQ ID NO:185, SEQ ID NO:187, SEQ ID NO:189, SEQ ID NO:191, SEQ ID NO:193, SEQ ID NO:195, SEQ ID NO:197, SEQ ID NO:199, SEQ ID NO:201, SEQ ID NO:203, SEQ ID NO:205, SEQ ID NO:207, SEQ ID NO:209, SEQ ID NO:211, SEQ ID NO:213, SEQ ID NO:215, SEQ ID NO:217, SEQ ID NO:219, SEQ ID NO:221, SEQ ID NO:223, SEQ ID NO:225, SEQ ID NO:227, SEQ ID NO:229,
25 SEQ ID NO:231, SEQ ID NO:233, SEQ ID NO:235, SEQ ID NO:237, SEQ ID NO:239, SEQ ID NO:241, SEQ ID NO:243, SEQ ID NO:245, SEQ ID NO:247, SEQ ID NO:249, SEQ ID NO:251, SEQ ID NO:253, SEQ ID NO:255, SEQ ID NO:257, SEQ ID NO:259, SEQ ID NO:261, SEQ ID NO:263, SEQ ID NO:265, SEQ ID NO:267, SEQ ID NO:269, SEQ ID NO:271, SEQ ID NO:273, SEQ ID NO:275, SEQ ID NO:277, SEQ ID NO:279,
30 SEQ ID NO:281, SEQ ID NO:283, SEQ ID NO:285, SEQ ID NO:287, SEQ ID NO:289, SEQ ID NO:291, SEQ ID NO:293, SEQ ID NO:295, SEQ ID NO:297, SEQ ID NO:299, SEQ ID NO:301, SEQ ID NO:303, SEQ ID NO:305, SEQ ID NO:307, SEQ ID NO:309, SEQ ID NO:311, SEQ ID NO:313, SEQ ID NO:315, SEQ ID NO:317, SEQ ID NO:319, SEQ ID NO:321, SEQ ID NO:323, SEQ ID NO:325, SEQ ID NO:327, SEQ ID NO:329,

SEQ ID NO:331, SEQ ID NO:333, SEQ ID NO:335, SEQ ID NO:337, SEQ ID NO:339,
SEQ ID NO:341, SEQ ID NO:343, SEQ ID NO:345, SEQ ID NO:347, SEQ ID NO:349,
SEQ ID NO:351, SEQ ID NO:353, SEQ ID NO:355, SEQ ID NO:357, SEQ ID NO:359,
SEQ ID NO:361, SEQ ID NO:363, SEQ ID NO:365, SEQ ID NO:367, SEQ ID NO:369,
5 SEQ ID NO:371, SEQ ID NO:373, SEQ ID NO:375, SEQ ID NO:377 or SEQ ID NO:379,
wherein the nucleic acid encodes a polypeptide having a xylanase activity.

25. The isolated or recombinant nucleic acid of claim 24, wherein the
nucleic acid is at least about 50, 75, 100, 150, 200, 300, 400, 500, 600, 700, 800, 900, 1000 or
10 more residues in length or the full length of the gene or transcript.

26. The isolated or recombinant nucleic acid of claim 24, wherein the
stringent conditions include a wash step comprising a wash in 0.2X SSC at a temperature of
about 65°C for about 15 minutes.

15 27. A nucleic acid probe for identifying a nucleic acid encoding a
polypeptide with a xylanase activity, wherein the probe comprises at least 10 consecutive
bases of a sequence comprising SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7,
SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, SEQ ID
20 NO:19, SEQ ID NO:21, SEQ ID NO:23, SEQ ID NO:25, SEQ ID NO:27, SEQ ID NO:29,
SEQ ID NO:31, SEQ ID NO:33, SEQ ID NO:35, SEQ ID NO:37, SEQ ID NO:39, SEQ ID
NO:41, SEQ ID NO:43, SEQ ID NO:45, SEQ ID NO:47, SEQ ID NO:49, SEQ ID NO:51,
SEQ ID NO:53, SEQ ID NO:55, SEQ ID NO:57, SEQ ID NO:59, SEQ ID NO:61, SEQ ID
NO:63, SEQ ID NO:65, SEQ ID NO:67, SEQ ID NO:69, SEQ ID NO:71, SEQ ID NO:73,
25 SEQ ID NO:75, SEQ ID NO:77, SEQ ID NO:79, SEQ ID NO:81, SEQ ID NO:83, SEQ ID
NO:85, SEQ ID NO:87, SEQ ID NO:89, SEQ ID NO:91, SEQ ID NO:93, SEQ ID NO:95,
SEQ ID NO:97, SEQ ID NO:99, SEQ ID NO:101, SEQ ID NO:103, SEQ ID NO:105, SEQ
ID NO:107, SEQ ID NO:109, SEQ ID NO:111, SEQ ID NO:113, SEQ ID NO:115, SEQ ID
NO:117, SEQ ID NO:119, SEQ ID NO:121, SEQ ID NO:123, SEQ ID NO:125, SEQ ID
30 NO:127, SEQ ID NO:129, SEQ ID NO:131, SEQ ID NO:133, SEQ ID NO:135, SEQ ID
NO:137, SEQ ID NO:139, SEQ ID NO:141, SEQ ID NO:143, SEQ ID NO:145, SEQ ID
NO:147, SEQ ID NO:149, SEQ ID NO:151, SEQ ID NO:153, SEQ ID NO:155, SEQ ID
NO:157, SEQ ID NO:199, SEQ ID NO:161, SEQ ID NO:163, SEQ ID NO:165, SEQ ID
NO:167, SEQ ID NO:169, SEQ ID NO:171, SEQ ID NO:173, SEQ ID NO:175, SEQ ID

NO:177, SEQ ID NO:179, SEQ ID NO:181, SEQ ID NO:183, SEQ ID NO:185, SEQ ID NO:187, SEQ ID NO:189, SEQ ID NO:191, SEQ ID NO:193, SEQ ID NO:195, SEQ ID NO:197, SEQ ID NO:199, SEQ ID NO:201, SEQ ID NO:203, SEQ ID NO:205, SEQ ID NO:207, SEQ ID NO:209, SEQ ID NO:211, SEQ ID NO:213, SEQ ID NO:215, SEQ ID NO:217, SEQ ID NO:219, SEQ ID NO:221, SEQ ID NO:223, SEQ ID NO:225, SEQ ID NO:227, SEQ ID NO:229, SEQ ID NO:231, SEQ ID NO:233, SEQ ID NO:235, SEQ ID NO:237, SEQ ID NO:239, SEQ ID NO:241, SEQ ID NO:243, SEQ ID NO:245, SEQ ID NO:247, SEQ ID NO:249, SEQ ID NO:251, SEQ ID NO:253, SEQ ID NO:255, SEQ ID NO:257, SEQ ID NO:259, SEQ ID NO:261, SEQ ID NO:263, SEQ ID NO:265, SEQ ID NO:267, SEQ ID NO:269, SEQ ID NO:271, SEQ ID NO:273, SEQ ID NO:275, SEQ ID NO:277, SEQ ID NO:279, SEQ ID NO:281, SEQ ID NO:283, SEQ ID NO:285, SEQ ID NO:287, SEQ ID NO:289, SEQ ID NO:291, SEQ ID NO:293, SEQ ID NO:295, SEQ ID NO:297, SEQ ID NO:299, SEQ ID NO:301, SEQ ID NO:303, SEQ ID NO:305, SEQ ID NO:307, SEQ ID NO:309, SEQ ID NO:311, SEQ ID NO:313, SEQ ID NO:315, SEQ ID NO:317, SEQ ID NO:319, SEQ ID NO:321, SEQ ID NO:323, SEQ ID NO:325, SEQ ID NO:327, SEQ ID NO:329, SEQ ID NO:331, SEQ ID NO:333, SEQ ID NO:335, SEQ ID NO:337, SEQ ID NO:339, SEQ ID NO:341, SEQ ID NO:343, SEQ ID NO:345, SEQ ID NO:347, SEQ ID NO:349, SEQ ID NO:351, SEQ ID NO:353, SEQ ID NO:355, SEQ ID NO:357, SEQ ID NO:359, SEQ ID NO:361, SEQ ID NO:363, SEQ ID NO:365, SEQ ID NO:367, SEQ ID NO:369, SEQ ID NO:371, SEQ ID NO:373, SEQ ID NO:375, SEQ ID NO:377 or SEQ ID NO:379, wherein the probe identifies the nucleic acid by binding or hybridization.

28. The nucleic acid probe of claim 27, wherein the probe comprises an oligonucleotide comprising at least about 10 to 50, about 20 to 60, about 30 to 70, about 40 to 80, about 60 to 100, or about 50 to 150 consecutive bases.

29. A nucleic acid probe for identifying a nucleic acid encoding a polypeptide having a xylanase activity, wherein the probe comprises a nucleic acid comprising at least about 10 consecutive residues of a nucleic acid sequence having at least 50% sequence identity to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, SEQ ID NO:23, SEQ ID NO:25, SEQ ID NO:27, SEQ ID NO:29, SEQ ID NO:31, SEQ ID NO:33, SEQ ID NO:35, SEQ ID NO:37, SEQ ID NO:39, SEQ ID NO:41,

SEQ ID NO:43, SEQ ID NO:45, SEQ ID NO:47, SEQ ID NO:49, SEQ ID NO:51, SEQ ID
NO:53, SEQ ID NO:55, SEQ ID NO:57, SEQ ID NO:59, SEQ ID NO:61, SEQ ID NO:63,
SEQ ID NO:65, SEQ ID NO:67, SEQ ID NO:69, SEQ ID NO:71, SEQ ID NO:73, SEQ ID
NO:75, SEQ ID NO:77, SEQ ID NO:79, SEQ ID NO:81, SEQ ID NO:83, SEQ ID NO:85,
5 SEQ ID NO:87, SEQ ID NO:89, SEQ ID NO:91, SEQ ID NO:93, SEQ ID NO:95, SEQ ID
NO:97, SEQ ID NO:99, SEQ ID NO:101, SEQ ID NO:103, SEQ ID NO:105, SEQ ID
NO:107, SEQ ID NO:109, SEQ ID NO:111, SEQ ID NO:113, SEQ ID NO:115, SEQ ID
NO:117, SEQ ID NO:119, SEQ ID NO:121, SEQ ID NO:123, SEQ ID NO:125, SEQ ID
NO:127, SEQ ID NO:129, SEQ ID NO:131, SEQ ID NO:133, SEQ ID NO:135, SEQ ID
10 NO:137, SEQ ID NO:139, SEQ ID NO:141, SEQ ID NO:143, SEQ ID NO:145, SEQ ID
NO:147, SEQ ID NO:149, SEQ ID NO:151, SEQ ID NO:153, SEQ ID NO:155, SEQ ID
NO:157, SEQ ID NO:199, SEQ ID NO:161, SEQ ID NO:163, SEQ ID NO:165, SEQ ID
NO:167, SEQ ID NO:169, SEQ ID NO:171, SEQ ID NO:173, SEQ ID NO:175, SEQ ID
NO:177, SEQ ID NO:179, SEQ ID NO:181, SEQ ID NO:183, SEQ ID NO:185, SEQ ID
15 NO:187, SEQ ID NO:189, SEQ ID NO:191, SEQ ID NO:193, SEQ ID NO:195, SEQ ID
NO:197, SEQ ID NO:199, SEQ ID NO:201, SEQ ID NO:203, SEQ ID NO:205, SEQ ID
NO:207, SEQ ID NO:209, SEQ ID NO:211, SEQ ID NO:213, SEQ ID NO:215, SEQ ID
NO:217, SEQ ID NO:219, SEQ ID NO:221, SEQ ID NO:223, SEQ ID NO:225, SEQ ID
NO:227, SEQ ID NO:229, SEQ ID NO:231, SEQ ID NO:233, SEQ ID NO:235, SEQ ID
20 NO:237, SEQ ID NO:239, SEQ ID NO:241, SEQ ID NO:243, SEQ ID NO:245, SEQ ID
NO:247, SEQ ID NO:249, SEQ ID NO:251, SEQ ID NO:253, SEQ ID NO:255, SEQ ID
NO:257, SEQ ID NO:259, SEQ ID NO:261, SEQ ID NO:263, SEQ ID NO:265, SEQ ID
NO:267, SEQ ID NO:269, SEQ ID NO:271, SEQ ID NO:273, SEQ ID NO:275, SEQ ID
NO:277, SEQ ID NO:279, SEQ ID NO:281, SEQ ID NO:283, SEQ ID NO:285, SEQ ID
25 NO:287, SEQ ID NO:289, SEQ ID NO:291, SEQ ID NO:293, SEQ ID NO:295, SEQ ID
NO:297, SEQ ID NO:299, SEQ ID NO:301, SEQ ID NO:303, SEQ ID NO:305, SEQ ID
NO:307, SEQ ID NO:309, SEQ ID NO:311, SEQ ID NO:313, SEQ ID NO:315, SEQ ID
NO:317, SEQ ID NO:319, SEQ ID NO:321, SEQ ID NO:323, SEQ ID NO:325, SEQ ID
NO:327, SEQ ID NO:329, SEQ ID NO:331, SEQ ID NO:333, SEQ ID NO:335, SEQ ID
30 NO:337, SEQ ID NO:339, SEQ ID NO:341, SEQ ID NO:343, SEQ ID NO:345, SEQ ID
NO:347, SEQ ID NO:349, SEQ ID NO:351, SEQ ID NO:353, SEQ ID NO:355, SEQ ID
NO:357, SEQ ID NO:359, SEQ ID NO:361, SEQ ID NO:363, SEQ ID NO:365, SEQ ID
NO:367, SEQ ID NO:369, SEQ ID NO:371, SEQ ID NO:373, SEQ ID NO:375, SEQ ID

NO:377 or SEQ ID NO:379, wherein the sequence identities are determined by analysis with a sequence comparison algorithm or by visual inspection.

30. The nucleic acid probe of claim 29, wherein the probe comprises an
5 oligonucleotide comprising at least about 10 to 50, about 20 to 60, about 30 to 70, about 40 to 80, about 60 to 100, or about 50 to 150 consecutive bases.

31. An amplification primer pair for amplifying a nucleic acid encoding a
polypeptide having a xylanase activity, wherein the primer pair is capable of amplifying a
10 nucleic acid comprising a sequence as set forth in claim 1 or claim 24, or a subsequence thereof.

32. The amplification primer pair of claim 31, wherein a member of the
amplification primer sequence pair comprises an oligonucleotide comprising at least about 10
15 to 50 consecutive bases of the sequence, or, about 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30 or more consecutive bases of the sequence.

33. An amplification primer pair, wherein the primer pair comprises a first
member having a sequence as set forth by about the first (the 5') 12, 13, 14, 15, 16, 17, 18,
20 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30 or more residues of SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, SEQ ID NO:23, SEQ ID NO:25, SEQ ID NO:27, SEQ ID NO:29, SEQ ID NO:31, SEQ ID NO:33, SEQ ID NO:35, SEQ ID NO:37, SEQ ID NO:39, SEQ ID NO:41, SEQ ID NO:43, SEQ ID NO:45, SEQ ID NO:47,
25 SEQ ID NO:49, SEQ ID NO:51, SEQ ID NO:53, SEQ ID NO:55, SEQ ID NO:57, SEQ ID NO:59, SEQ ID NO:61, SEQ ID NO:63, SEQ ID NO:65, SEQ ID NO:67, SEQ ID NO:69, SEQ ID NO:71, SEQ ID NO:73, SEQ ID NO:75, SEQ ID NO:77, SEQ ID NO:79, SEQ ID NO:81, SEQ ID NO:83, SEQ ID NO:85, SEQ ID NO:87, SEQ ID NO:89, SEQ ID NO:91, SEQ ID NO:93, SEQ ID NO:95, SEQ ID NO:97, SEQ ID NO:99, SEQ ID NO:101, SEQ ID NO:103, SEQ ID NO:105, SEQ ID NO:107, SEQ ID NO:109, SEQ ID NO:111, SEQ ID NO:113, SEQ ID NO:115, SEQ ID NO:117, SEQ ID NO:119, SEQ ID NO:121, SEQ ID NO:123, SEQ ID NO:125, SEQ ID NO:127, SEQ ID NO:129, SEQ ID NO:131, SEQ ID NO:133, SEQ ID NO:135, SEQ ID NO:137, SEQ ID NO:139, SEQ ID NO:141, SEQ ID NO:143, SEQ ID NO:145, SEQ ID NO:147, SEQ ID NO:149, SEQ ID NO:151, SEQ ID

NO:153, SEQ ID NO:155, SEQ ID NO:157, SEQ ID NO:199, SEQ ID NO:161, SEQ ID
 NO:163, SEQ ID NO:165, SEQ ID NO:167, SEQ ID NO:169, SEQ ID NO:171, SEQ ID
 NO:173, SEQ ID NO:175, SEQ ID NO:177, SEQ ID NO:179, SEQ ID NO:181, SEQ ID
 NO:183, SEQ ID NO:185, SEQ ID NO:187, SEQ ID NO:189, SEQ ID NO:191, SEQ ID
 5 NO:193, SEQ ID NO:195, SEQ ID NO:197, SEQ ID NO:199, SEQ ID NO:201, SEQ ID
 NO:203, SEQ ID NO:205, SEQ ID NO:207, SEQ ID NO:209, SEQ ID NO:211, SEQ ID
 NO:213, SEQ ID NO:215, SEQ ID NO:217, SEQ ID NO:219, SEQ ID NO:221, SEQ ID
 NO:223, SEQ ID NO:225, SEQ ID NO:227, SEQ ID NO:229, SEQ ID NO:231, SEQ ID
 NO:233, SEQ ID NO:235, SEQ ID NO:237, SEQ ID NO:239, SEQ ID NO:241, SEQ ID
 10 NO:243, SEQ ID NO:245, SEQ ID NO:247, SEQ ID NO:249, SEQ ID NO:251, SEQ ID
 NO:253, SEQ ID NO:255, SEQ ID NO:257, SEQ ID NO:259, SEQ ID NO:261, SEQ ID
 NO:263, SEQ ID NO:265, SEQ ID NO:267, SEQ ID NO:269, SEQ ID NO:271, SEQ ID
 NO:273, SEQ ID NO:275, SEQ ID NO:277, SEQ ID NO:279, SEQ ID NO:281, SEQ ID
 NO:283, SEQ ID NO:285, SEQ ID NO:287, SEQ ID NO:289, SEQ ID NO:291, SEQ ID
 15 NO:293, SEQ ID NO:295, SEQ ID NO:297, SEQ ID NO:299, SEQ ID NO:301, SEQ ID
 NO:303, SEQ ID NO:305, SEQ ID NO:307, SEQ ID NO:309, SEQ ID NO:311, SEQ ID
 NO:313, SEQ ID NO:315, SEQ ID NO:317, SEQ ID NO:319, SEQ ID NO:321, SEQ ID
 NO:323, SEQ ID NO:325, SEQ ID NO:327, SEQ ID NO:329, SEQ ID NO:331, SEQ ID
 NO:333, SEQ ID NO:335, SEQ ID NO:337, SEQ ID NO:339, SEQ ID NO:341, SEQ ID
 20 NO:343, SEQ ID NO:345, SEQ ID NO:347, SEQ ID NO:349, SEQ ID NO:351, SEQ ID
 NO:353, SEQ ID NO:355, SEQ ID NO:357, SEQ ID NO:359, SEQ ID NO:361, SEQ ID
 NO:363, SEQ ID NO:365, SEQ ID NO:367, SEQ ID NO:369, SEQ ID NO:371, SEQ ID
 NO:373, SEQ ID NO:375, SEQ ID NO:377 or SEQ ID NO:379, and a second member
 having a sequence as set forth by about the first (the 5') 12, 13, 14, 15, 16, 17, 18, 19, 20, 21,
 25 22, 23, 24, 25, 26, 27, 28, 29, 30 or more residues of the complementary strand of the first
 member.

34. A xylanase-encoding nucleic acid generated by amplification of a
 polynucleotide using an amplification primer pair as set forth in claim 33.

30

35. The xylanase-encoding nucleic acid of claim 34, wherein the
 amplification is by polymerase chain reaction (PCR).

36. The xylanase-encoding nucleic acid of claim 34, wherein the nucleic acid generated by amplification of a gene library.

37. The xylanase-encoding nucleic acid of claim 34, wherein the gene library is an environmental library.

38. An isolated or recombinant xylanase encoded by a xylanase-encoding nucleic acid as set forth in claim 34.

39. A method of amplifying a nucleic acid encoding a polypeptide having a xylanase activity comprising amplification of a template nucleic acid with an amplification primer sequence pair capable of amplifying a nucleic acid sequence as set forth in claim 1 or claim 24, or a subsequence thereof.

40. An expression cassette comprising a nucleic acid comprising a sequence as set forth in claim 1 or claim 24.

41. A vector comprising a nucleic acid comprising a sequence as set forth in claim 1 or claim 24.

42. A cloning vehicle comprising a nucleic acid comprising a sequence as set forth in claim 1 or claim 24, wherein the cloning vehicle comprises a viral vector, a plasmid, a phage, a phagemid, a cosmid, a fosmid, a bacteriophage or an artificial chromosome.

43. The cloning vehicle of claim 42, wherein the viral vector comprises an adenovirus vector, a retroviral vector or an adeno-associated viral vector.

44. The cloning vehicle of claim 42, comprising a bacterial artificial chromosome (BAC), a plasmid, a bacteriophage P1-derived vector (PAC), a yeast artificial chromosome (YAC), or a mammalian artificial chromosome (MAC).

45. A transformed cell comprising a nucleic acid comprising a sequence as set forth in claim 1 or claim 24.

46. A transformed cell comprising an expression cassette as set forth in claim 40.

5 47. The transformed cell of claim 40, wherein the cell is a bacterial cell, a mammalian cell, a fungal cell, a yeast cell, an insect cell or a plant cell.

48. A transgenic non-human animal comprising a sequence as set forth in claim 1 or claim 24.

10 49. The transgenic non-human animal of claim 48, wherein the animal is a mouse.

15 50. A transgenic plant comprising a sequence as set forth in claim 1 or claim 24.

20 51. The transgenic plant of claim 50, wherein the plant is a corn plant, a sorghum plant, a potato plant, a tomato plant, a wheat plant, an oilseed plant, a rapeseed plant, a soybean plant, a rice plant, a barley plant, a grass, or a tobacco plant.

52. A transgenic seed comprising a sequence as set forth in claim 1 or claim 24.

25 53. The transgenic seed of claim 52, wherein the seed is a corn seed, a wheat kernel, an oilseed, a rapeseed, a soybean seed, a palm kernel, a sunflower seed, a sesame seed, a rice, a barley, a peanut or a tobacco plant seed.

30 54. An antisense oligonucleotide comprising a nucleic acid sequence complementary to or capable of hybridizing under stringent conditions to a sequence as set forth in claim 1 or claim 24, or a subsequence thereof.

55. The antisense oligonucleotide of claim 49, wherein the antisense oligonucleotide is between about 10 to 50, about 20 to 60, about 30 to 70, about 40 to 80, or about 60 to 100 bases in length.

56. A method of inhibiting the translation of a xylanase message in a cell comprising administering to the cell or expressing in the cell an antisense oligonucleotide comprising a nucleic acid sequence complementary to or capable of hybridizing under
5 stringent conditions to a sequence as set forth in claim 1 or claim 24.

57. A double-stranded inhibitory RNA (RNAi) molecule comprising a subsequence of a sequence as set forth in claim 1 or claim 24.

10 58. The double-stranded inhibitory RNA (RNAi) molecule of claim 52, wherein the RNAi is about 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25 or more duplex nucleotides in length.

59. A method of inhibiting the expression of a xylanase in a cell
15 comprising administering to the cell or expressing in the cell a double-stranded inhibitory RNA (iRNA), wherein the RNA comprises a subsequence of a sequence as set forth in claim 1 or claim 24.

60. An isolated or recombinant polypeptide (i) having at least 50%
20 sequence identity to SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:12, SEQ ID NO:14, SEQ ID NO:16, SEQ ID NO:18, SEQ ID NO:20, SEQ ID NO:22, SEQ ID NO:24, SEQ ID NO:26, SEQ ID NO:28, SEQ ID NO:30, SEQ ID NO:32, SEQ ID NO:34, SEQ ID NO:36, SEQ ID NO:38, SEQ ID NO:40, SEQ ID NO:42, SEQ ID NO:44, SEQ ID NO:46, SEQ ID NO:48, SEQ ID NO:50, SEQ ID NO:52, SEQ ID
25 NO:54, SEQ ID NO:56, SEQ ID NO:58, SEQ ID NO:60, SEQ ID NO:62, SEQ ID NO:64, SEQ ID NO:66, SEQ ID NO:68, SEQ ID NO:70, SEQ ID NO:72, SEQ ID NO:74, SEQ ID NO:76, SEQ ID NO:78, SEQ ID NO:80, SEQ ID NO:82, SEQ ID NO:84, SEQ ID NO:86, SEQ ID NO:88, SEQ ID NO:90, SEQ ID NO:92, SEQ ID NO:94, SEQ ID NO:96, SEQ ID NO:98, SEQ ID NO:100, SEQ ID NO:102, SEQ ID NO:104, SEQ ID NO:106, SEQ ID
30 NO:108, SEQ ID NO:110, SEQ ID NO:112, SEQ ID NO:114, SEQ ID NO:116, SEQ ID NO:118, SEQ ID NO:120, SEQ ID NO:122, SEQ ID NO:124, SEQ ID NO:126, SEQ ID NO:128, SEQ ID NO:130, SEQ ID NO:132, SEQ ID NO:134, SEQ ID NO:136, SEQ ID NO:138, SEQ ID NO:140, SEQ ID NO:142, SEQ ID NO:144, SEQ ID NO:146, SEQ ID NO:148, SEQ ID NO:150, SEQ ID NO:152, SEQ ID NO:154, SEQ ID NO:156, SEQ ID NO:158,

SEQ ID NO:160, SEQ ID NO:162, SEQ ID NO:164, SEQ ID NO:166, SEQ ID NO:168,
SEQ ID NO:170, SEQ ID NO:172, SEQ ID NO:174, SEQ ID NO:176, SEQ ID NO:178,
SEQ ID NO:180, SEQ ID NO:182, SEQ ID NO:184, SEQ ID NO:186, SEQ ID NO:188,
SEQ ID NO:190, SEQ ID NO:192, SEQ ID NO:194, SEQ ID NO:196, SEQ ID NO:198,
5 SEQ ID NO:200, SEQ ID NO:202, SEQ ID NO:204, SEQ ID NO:206, SEQ ID NO:208,
SEQ ID NO:210, SEQ ID NO:212, SEQ ID NO:214, SEQ ID NO:216, SEQ ID NO:218,
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SEQ ID NO:240, SEQ ID NO:242, SEQ ID NO:244, SEQ ID NO:246, SEQ ID NO:248,
10 SEQ ID NO:250, SEQ ID NO:252, SEQ ID NO:254, SEQ ID NO:256, SEQ ID NO:258,
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15 SEQ ID NO:300, SEQ ID NO:302, SEQ ID NO:304, SEQ ID NO:306, SEQ ID NO:308,
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SEQ ID NO:330, SEQ ID NO:332, SEQ ID NO:334, SEQ ID NO:336, SEQ ID NO:338,
SEQ ID NO:340, SEQ ID NO:342, SEQ ID NO:344, SEQ ID NO:346, SEQ ID NO:348,
20 SEQ ID NO:350, SEQ ID NO:352, SEQ ID NO:354, SEQ ID NO:356, SEQ ID NO:358,
SEQ ID NO:360, SEQ ID NO:362, SEQ ID NO:364, SEQ ID NO:366, SEQ ID NO:368,
SEQ ID NO:370, SEQ ID NO:372, SEQ ID NO:374, SEQ ID NO:376, SEQ ID NO:378 or
SEQ ID NO:380, over a region of at least about 100 residues, wherein the sequence identities
are determined by analysis with a sequence comparison algorithm or by a visual inspection,
25 or, (ii) encoded by a nucleic acid having at least 50% sequence identity to a sequence as set
forth in SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID
NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21,
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30 SEQ ID NO:45, SEQ ID NO:47, SEQ ID NO:49, SEQ ID NO:51, SEQ ID NO:53, SEQ ID
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NO:99, SEQ ID NO:101, SEQ ID NO:103, SEQ ID NO:105, SEQ ID NO:107, SEQ ID
NO:109, SEQ ID NO:111, SEQ ID NO:113, SEQ ID NO:115, SEQ ID NO:117, SEQ ID
NO:119, SEQ ID NO:121, SEQ ID NO:123, SEQ ID NO:125, SEQ ID NO:127, SEQ ID
NO:129, SEQ ID NO:131, SEQ ID NO:133, SEQ ID NO:135, SEQ ID NO:137, SEQ ID
5 NO:139, SEQ ID NO:141, SEQ ID NO:143, SEQ ID NO:145, SEQ ID NO:147, SEQ ID
NO:149, SEQ ID NO:151, SEQ ID NO:153, SEQ ID NO:155, SEQ ID NO:157, SEQ ID
NO:199, SEQ ID NO:161, SEQ ID NO:163, SEQ ID NO:165, SEQ ID NO:167, SEQ ID
NO:169, SEQ ID NO:171, SEQ ID NO:173, SEQ ID NO:175, SEQ ID NO:177, SEQ ID
NO:179, SEQ ID NO:181, SEQ ID NO:183, SEQ ID NO:185, SEQ ID NO:187, SEQ ID
10 NO:189, SEQ ID NO:191, SEQ ID NO:193, SEQ ID NO:195, SEQ ID NO:197, SEQ ID
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NO:209, SEQ ID NO:211, SEQ ID NO:213, SEQ ID NO:215, SEQ ID NO:217, SEQ ID
NO:219, SEQ ID NO:221, SEQ ID NO:223, SEQ ID NO:225, SEQ ID NO:227, SEQ ID
NO:229, SEQ ID NO:231, SEQ ID NO:233, SEQ ID NO:235, SEQ ID NO:237, SEQ ID
15 NO:239, SEQ ID NO:241, SEQ ID NO:243, SEQ ID NO:245, SEQ ID NO:247, SEQ ID
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NO:269, SEQ ID NO:271, SEQ ID NO:273, SEQ ID NO:275, SEQ ID NO:277, SEQ ID
NO:279, SEQ ID NO:281, SEQ ID NO:283, SEQ ID NO:285, SEQ ID NO:287, SEQ ID
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NO:329, SEQ ID NO:331, SEQ ID NO:333, SEQ ID NO:335, SEQ ID NO:337, SEQ ID
25 NO:339, SEQ ID NO:341, SEQ ID NO:343, SEQ ID NO:345, SEQ ID NO:347, SEQ ID
NO:349, SEQ ID NO:351, SEQ ID NO:353, SEQ ID NO:355, SEQ ID NO:357, SEQ ID
NO:359, SEQ ID NO:361, SEQ ID NO:363, SEQ ID NO:365, SEQ ID NO:367, SEQ ID
NO:369, SEQ ID NO:371, SEQ ID NO:373, SEQ ID NO:375, SEQ ID NO:377 or SEQ ID
NO:379, over a region of at least about 100 residues, and the sequence identities are
30 determined by analysis with a sequence comparison algorithm or by a visual inspection, or
encoded by a nucleic acid capable of hybridizing under stringent conditions to a sequence as
set forth in SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ
ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21,
SEQ ID NO:23, SEQ ID NO:25, SEQ ID NO:27, SEQ ID NO:29, SEQ ID NO:31, SEQ ID

NO:33, SEQ ID NO:35, SEQ ID NO:37, SEQ ID NO:39, SEQ ID NO:41, SEQ ID NO:43,
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NO:55, SEQ ID NO:57, SEQ ID NO:59, SEQ ID NO:61, SEQ ID NO:63, SEQ ID NO:65,
SEQ ID NO:67, SEQ ID NO:69, SEQ ID NO:71, SEQ ID NO:73, SEQ ID NO:75, SEQ ID
5 NO:77, SEQ ID NO:79, SEQ ID NO:81, SEQ ID NO:83, SEQ ID NO:85, SEQ ID NO:87,
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NO:139, SEQ ID NO:141, SEQ ID NO:143, SEQ ID NO:145, SEQ ID NO:147, SEQ ID
NO:149, SEQ ID NO:151, SEQ ID NO:153, SEQ ID NO:155, SEQ ID NO:157, SEQ ID
NO:199, SEQ ID NO:161, SEQ ID NO:163, SEQ ID NO:165, SEQ ID NO:167, SEQ ID
NO:169, SEQ ID NO:171, SEQ ID NO:173, SEQ ID NO:175, SEQ ID NO:177, SEQ ID
15 NO:179, SEQ ID NO:181, SEQ ID NO:183, SEQ ID NO:185, SEQ ID NO:187, SEQ ID
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NO:219, SEQ ID NO:221, SEQ ID NO:223, SEQ ID NO:225, SEQ ID NO:227, SEQ ID
20 NO:229, SEQ ID NO:231, SEQ ID NO:233, SEQ ID NO:235, SEQ ID NO:237, SEQ ID
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25 NO:279, SEQ ID NO:281, SEQ ID NO:283, SEQ ID NO:285, SEQ ID NO:287, SEQ ID
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30 NO:329, SEQ ID NO:331, SEQ ID NO:333, SEQ ID NO:335, SEQ ID NO:337, SEQ ID
NO:339, SEQ ID NO:341, SEQ ID NO:343, SEQ ID NO:345, SEQ ID NO:347, SEQ ID
NO:349, SEQ ID NO:351, SEQ ID NO:353, SEQ ID NO:355, SEQ ID NO:357, SEQ ID
NO:359, SEQ ID NO:361, SEQ ID NO:363, SEQ ID NO:365, SEQ ID NO:367, SEQ ID

NO:369, SEQ ID NO:371, SEQ ID NO:373, SEQ ID NO:375, SEQ ID NO:377 or SEQ ID NO:379.

61. The isolated or recombinant polypeptide of claim 60, wherein the
5 sequence identity is over a region of at least about 51%, 52%, 53%, 54%, 55%,
56%, 57%, 58%, 59%, 60%, 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, 70%, 71%,
72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%,
88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or more, or is 100%
sequence identity.

62. The isolated or recombinant polypeptide of claim 60, wherein the
10 sequence identity is over a region of at least about 10, 15, 20, 25, 30, 35, 40, 45, 50, 75, 100,
150, 200, 250, 300, 350, 400, 450, 500, 550, 600, 650, 700, 750, 800, 850, 900, 950, 1000,
1050 or more residues, or the full length of an enzyme.

63. The isolated or recombinant polypeptide of claim 60, wherein the
polypeptide has a sequence as set forth in SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ
ID NO:8, SEQ ID NO:10, SEQ ID NO:12, SEQ ID NO:14, SEQ ID NO:16, SEQ ID NO:18,
SEQ ID NO:20, SEQ ID NO:22, SEQ ID NO:24, SEQ ID NO:26, SEQ ID NO:28, SEQ ID
20 NO:30, SEQ ID NO:32, SEQ ID NO:34, SEQ ID NO:36, SEQ ID NO:38, SEQ ID NO:40,
SEQ ID NO:42, SEQ ID NO:44, SEQ ID NO:46, SEQ ID NO:48, SEQ ID NO:50, SEQ ID
NO:52, SEQ ID NO:54, SEQ ID NO:56, SEQ ID NO:58, SEQ ID NO:60, SEQ ID NO:62,
SEQ ID NO:64, SEQ ID NO:66, SEQ ID NO:68, SEQ ID NO:70, SEQ ID NO:72, SEQ ID
NO:74, SEQ ID NO:76, SEQ ID NO:78, SEQ ID NO:80, SEQ ID NO:82, SEQ ID NO:84,
25 SEQ ID NO:86, SEQ ID NO:88, SEQ ID NO:90, SEQ ID NO:92, SEQ ID NO:94, SEQ ID
NO:96, SEQ ID NO:98, SEQ ID NO:100, SEQ ID NO:102, SEQ ID NO:104, SEQ ID
NO:106, SEQ ID NO:108, SEQ ID NO:110, SEQ ID NO:112, SEQ ID NO:114, SEQ ID
NO:116, SEQ ID NO:118, SEQ ID NO:120, SEQ ID NO:122, SEQ ID NO:124, SEQ ID
NO:126, SEQ ID NO:128, SEQ ID NO:130, SEQ ID NO:132, SEQ ID NO:134, SEQ ID
30 NO:136, SEQ ID NO:138, SEQ ID NO:140, SEQ ID NO:142, SEQ ID NO:144, SEQ ID NO:146,
SEQ ID NO:148, SEQ ID NO:150, SEQ ID NO:152, SEQ ID NO:154, SEQ ID NO:156,
SEQ ID NO:158, SEQ ID NO:160, SEQ ID NO:162, SEQ ID NO:164, SEQ ID NO:166,
SEQ ID NO:168, SEQ ID NO:170, SEQ ID NO:172, SEQ ID NO:174, SEQ ID NO:176,
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SEQ ID NO:188, SEQ ID NO:190, SEQ ID NO:192, SEQ ID NO:194, SEQ ID NO:196,
SEQ ID NO:198, SEQ ID NO:200, SEQ ID NO:202, SEQ ID NO:204, SEQ ID NO:206,
SEQ ID NO:208, SEQ ID NO:210, SEQ ID NO:212, SEQ ID NO:214, SEQ ID NO:216,
SEQ ID NO:218, SEQ ID NO:220, SEQ ID NO:222, SEQ ID NO:224, SEQ ID NO:226,
5 SEQ ID NO:228, SEQ ID NO:230, SEQ ID NO:232, SEQ ID NO:234, SEQ ID NO:236,
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SEQ ID NO:268, SEQ ID NO:270, SEQ ID NO:272, SEQ ID NO:274, SEQ ID NO:276,
10 SEQ ID NO:278, SEQ ID NO:280, SEQ ID NO:282, SEQ ID NO:284, SEQ ID NO:286,
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SEQ ID NO:318, SEQ ID NO:320, SEQ ID NO:322, SEQ ID NO:324, SEQ ID NO:326,
15 SEQ ID NO:328, SEQ ID NO:330, SEQ ID NO:332, SEQ ID NO:334, SEQ ID NO:336,
SEQ ID NO:338, SEQ ID NO:340, SEQ ID NO:342, SEQ ID NO:344, SEQ ID NO:346,
SEQ ID NO:348, SEQ ID NO:350, SEQ ID NO:352, SEQ ID NO:354, SEQ ID NO:356,
SEQ ID NO:358, SEQ ID NO:360, SEQ ID NO:362, SEQ ID NO:364, SEQ ID NO:366,
SEQ ID NO:368, SEQ ID NO:370, SEQ ID NO:372, SEQ ID NO:374, SEQ ID NO:376,
20 SEQ ID NO:378 or SEQ ID NO:380.

64. The isolated or recombinant polypeptide of claim 60, wherein the polypeptide has a xylanase activity.

25 65. The isolated or recombinant polypeptide of claim 64, wherein the xylanase activity comprises catalyzing hydrolysis of internal β -1,4-xylosidic linkages.

66. The isolated or recombinant polypeptide of claim 65, wherein the xylanase activity comprises an endo-1,4-beta-xylanase activity.

30 67. The isolated or recombinant polypeptide of claim 64, wherein the xylanase activity comprises hydrolyzing a xylan to produce a smaller molecular weight xylose and xyo-oligomer.

68. The isolated or recombinant polypeptide of claim 67, wherein the xylan comprises an arabinoxylan.

5 69. The isolated or recombinant polypeptide of claim 68, wherein the arabinoxylan comprises a water soluble arabinoxylan.

70. The isolated or recombinant polypeptide of claim 69, wherein the water soluble arabinoxylan comprises a dough or a bread product.

10 71. The isolated or recombinant polypeptide of claim 64, wherein the xylanase activity comprises hydrolyzing polysaccharides comprising 1,4- β -glycoside-linked D-xylopyranoses.

15 72. The isolated or recombinant polypeptide of claim 64, wherein the xylanase activity comprises hydrolyzing hemicelluloses.

20 73. The isolated or recombinant polypeptide of claim 72, wherein the xylanase activity comprises hydrolyzing hemicelluloses in a wood or paper pulp or a paper product.

74. The isolated or recombinant polypeptide of claim 73, wherein the xylanase activity comprises catalyzing hydrolysis of xylans in a feed or a food product.

25 75. The isolated or recombinant polypeptide of claim 74, wherein the feed or food product comprises a cereal-based animal feed, a wort or a beer, a milk or a milk product, a fruit or a vegetable.

30 76. The isolated or recombinant polypeptide of claim 64, wherein the xylanase activity comprises catalyzing hydrolysis of xylans in a microbial cell or a plant cell.

77. The isolated or recombinant polypeptide of claim 64, wherein the xylanase activity is thermostable.

78. The isolated or recombinant polypeptide of claim 77, wherein the polypeptide retains a xylanase activity under conditions comprising a temperature range of between about 1°C to about 5°C, between about 5°C to about 15°C, between about 15°C to about 25°C, between about 25°C to about 37°C, between about 37°C to about 95°C, between
5 about 55°C to about 85°C, between about 70°C to about 95°C, between about 70°C to about 75°C, or between about 90°C to about 95°C.

79. The isolated or recombinant polypeptide of claim 64, wherein the xylanase activity is thermotolerant.
10

80. The isolated or recombinant polypeptide of claim 79, wherein the polypeptide retains a xylanase activity after exposure to a temperature in the range from between about 1°C to about 5°C, between about 5°C to about 15°C, between about 15°C to about 25°C, between about 25°C to about 37°C, between about 37°C to about 95°C, between
15 about 55°C to about 85°C, between about 70°C to about 75°C, or between about 90°C to about 95°C, or more.

81. An isolated or recombinant polypeptide comprising a polypeptide as set forth in claim 60 and lacking a signal sequence or a prepro sequence.
20

82. An isolated or recombinant polypeptide comprising a polypeptide as set forth in claim 60 and having a heterologous signal sequence or a heterologous prepro sequence.

83. The isolated or recombinant polypeptide of claim 64, wherein the xylanase activity comprises a specific activity at about 37°C in the range from about 100 to about 1000 units per milligram of protein, from about 500 to about 750 units per milligram of protein, from about 500 to about 1200 units per milligram of protein, or from about 750 to about 1000 units per milligram of protein.
25

84. The isolated or recombinant polypeptide of claim 79, wherein the thermotolerance comprises retention of at least half of the specific activity of the xylanase at 37°C after being heated to an elevated temperature.
30

85. The isolated or recombinant polypeptide of claim 79, wherein the thermotolerance comprises retention of specific activity at 37°C in the range from about 500 to about 1200 units per milligram of protein after being heated to an elevated temperature.

5 86. The isolated or recombinant polypeptide of claim 60, wherein the polypeptide comprises at least one glycosylation site.

87. The isolated or recombinant polypeptide of claim 86, wherein the glycosylation is an N-linked glycosylation.

10 88. The isolated or recombinant polypeptide of claim 87, wherein the polypeptide is glycosylated after being expressed in a *P. pastoris* or a *S. pombe*.

89. The isolated or recombinant polypeptide of claim 64, wherein the polypeptide retains a xylanase activity under conditions comprising about pH 6.5, pH 6.0, pH 5.5, 5.0, pH 4.5 or 4.0.

15 90. The isolated or recombinant polypeptide of claim 64, wherein the polypeptide retains a xylanase activity under conditions comprising about pH 7.5, pH 8.0, pH 8.5, pH 9, pH 9.5, pH 10 or pH 10.5.

91. A protein preparation comprising a polypeptide as set forth in claim 60, wherein the protein preparation comprises a liquid, a solid or a gel.

25 92. A heterodimer comprising a polypeptide as set forth in claim 60 and a second domain.

93. The heterodimer of claim 92, wherein the second domain is a polypeptide and the heterodimer is a fusion protein.

30 94. The heterodimer of claim 92, wherein the second domain is an epitope or a tag.

95. A homodimer comprising a polypeptide as set forth in claim 60.

96. An immobilized polypeptide, wherein the polypeptide comprises a sequence as set forth in claim 60, or a subsequence thereof.

5 97. The immobilized polypeptide of claim 96, wherein the polypeptide is immobilized on a cell, a metal, a resin, a polymer, a ceramic, a glass, a microelectrode, a graphitic particle, a bead, a gel, a plate, an array or a capillary tube.

10 98. An array comprising an immobilized polypeptide as set forth in claim 60.

99. An array comprising an immobilized nucleic acid as set forth in claim 1 or claim 24.

15 100. An isolated or recombinant antibody that specifically binds to a polypeptide as set forth in claim 60.

20 101. The isolated or recombinant antibody of claim 100, wherein the antibody is a monoclonal or a polyclonal antibody.

102. A hybridoma comprising an antibody that specifically binds to a polypeptide as set forth in claim 60.

25 103. A method of isolating or identifying a polypeptide with a xylanase activity comprising the steps of:

(a) providing an antibody as set forth in claim 100;
(b) providing a sample comprising polypeptides; and
(c) contacting the sample of step (b) with the antibody of step (a) under conditions wherein the antibody can specifically bind to the polypeptide, thereby isolating or
30 identifying a polypeptide having a xylanase activity.

104. A method of making an anti-xylanase antibody comprising administering to a non-human animal a nucleic acid as set forth in claim 1 or claim 24 or a

subsequence thereof in an amount sufficient to generate a humoral immune response, thereby making an anti-xylanase antibody.

105. A method of making an anti-xylanase antibody comprising
5 administering to a non-human animal a polypeptide as set forth in claim 60 or a subsequence thereof in an amount sufficient to generate a humoral immune response, thereby making an anti-xylanase antibody.

106. A method of producing a recombinant polypeptide comprising the
10 steps of: (a) providing a nucleic acid operably linked to a promoter, wherein the nucleic acid comprises a sequence as set forth in claim 1 or claim 24; and (b) expressing the nucleic acid of step (a) under conditions that allow expression of the polypeptide, thereby producing a recombinant polypeptide.

15 107. The method of claim 106, further comprising transforming a host cell with the nucleic acid of step (a) followed by expressing the nucleic acid of step (a), thereby producing a recombinant polypeptide in a transformed cell.

108. A method for identifying a polypeptide having a xylanase activity
20 comprising the following steps:
(a) providing a polypeptide as set forth in claim 64;
(b) providing a xylanase substrate; and
(c) contacting the polypeptide with the substrate of step (b) and detecting a decrease in the amount of substrate or an increase in the amount of a reaction product,
25 wherein a decrease in the amount of the substrate or an increase in the amount of the reaction product detects a polypeptide having a xylanase activity.

109. A method for identifying a xylanase substrate comprising the
following steps:
30 (a) providing a polypeptide as set forth in claim 64;
(b) providing a test substrate; and
(c) contacting the polypeptide of step (a) with the test substrate of step (b) and detecting a decrease in the amount of substrate or an increase in the amount of reaction

product, wherein a decrease in the amount of the substrate or an increase in the amount of a reaction product identifies the test substrate as a xylanase substrate.

5 110. A method of determining whether a test compound specifically binds to a polypeptide comprising the following steps:

(a) expressing a nucleic acid or a vector comprising the nucleic acid under conditions permissive for translation of the nucleic acid to a polypeptide, wherein the nucleic acid has a sequence as set forth in claim 1 or claim 24;

(b) providing a test compound;

10 (c) contacting the polypeptide with the test compound; and

(d) determining whether the test compound of step (b) specifically binds to the polypeptide.

15 111. A method of determining whether a test compound specifically binds to a polypeptide comprising the following steps:

(a) providing a polypeptide as set forth in claim 60;

(b) providing a test compound;

(c) contacting the polypeptide with the test compound; and

20 (d) determining whether the test compound of step (b) specifically binds to the polypeptide.

112. A method for identifying a modulator of a xylanase activity comprising the following steps:

(a) providing a polypeptide as set forth in claim 64;

25 (b) providing a test compound;

(c) contacting the polypeptide of step (a) with the test compound of step (b) and measuring an activity of the xylanase, wherein a change in the xylanase activity measured in the presence of the test compound compared to the activity in the absence of the test compound provides a determination that the test compound modulates the xylanase activity.

30

113. The method of claim 112, wherein the xylanase activity is measured by providing a xylanase substrate and detecting a decrease in the amount of the substrate or an

increase in the amount of a reaction product, or, an increase in the amount of the substrate or a decrease in the amount of a reaction product.

5 114. The method of claim 113, wherein a decrease in the amount of the substrate or an increase in the amount of the reaction product with the test compound as compared to the amount of substrate or reaction product without the test compound identifies the test compound as an activator of a xylanase activity.

10 115. The method of claim 113, wherein an increase in the amount of the substrate or a decrease in the amount of the reaction product with the test compound as compared to the amount of substrate or reaction product without the test compound identifies the test compound as an inhibitor of a xylanase activity.

15 116. A computer system comprising a processor and a data storage device wherein said data storage device has stored thereon a polypeptide sequence or a nucleic acid sequence, wherein the polypeptide sequence comprises sequence as set forth in claim 60, a polypeptide encoded by a nucleic acid as set forth in claim 1 or claim 24.

20 117. The computer system of claim 115, further comprising a sequence comparison algorithm and a data storage device having at least one reference sequence stored thereon.

25 118. The computer system of claim 117, wherein the sequence comparison algorithm comprises a computer program that indicates polymorphisms.

119. The computer system of claim 117, further comprising an identifier that identifies one or more features in said sequence.

30 120. A computer readable medium having stored thereon a polypeptide sequence or a nucleic acid sequence, wherein the polypeptide sequence comprises a polypeptide as set forth in claim 60; a polypeptide encoded by a nucleic acid as set forth in claim 1 or claim 24.

121. A method for identifying a feature in a sequence comprising the steps of: (a) reading the sequence using a computer program which identifies one or more features in a sequence, wherein the sequence comprises a polypeptide sequence or a nucleic acid sequence, wherein the polypeptide sequence comprises a polypeptide as set forth in claim 60; a polypeptide encoded by a nucleic acid as set forth in claim 1 or claim 24; and (b) identifying one or more features in the sequence with the computer program.

122. A method for comparing a first sequence to a second sequence comprising the steps of: (a) reading the first sequence and the second sequence through use of a computer program which compares sequences, wherein the first sequence comprises a polypeptide sequence or a nucleic acid sequence, wherein the polypeptide sequence comprises a polypeptide as set forth in claim 60 or a polypeptide encoded by a nucleic acid as set forth in claim 1 or claim 24; and (b) determining differences between the first sequence and the second sequence with the computer program.

123. The method of claim 122, wherein the step of determining differences between the first sequence and the second sequence further comprises the step of identifying polymorphisms.

124. The method of claim 123, further comprising an identifier that identifies one or more features in a sequence.

125. The method of claim 124, comprising reading the first sequence using a computer program and identifying one or more features in the sequence.

126. A method for isolating or recovering a nucleic acid encoding a polypeptide with a xylanase activity from an environmental sample comprising the steps of:
(a) providing an amplification primer sequence pair as set forth in claim 31 or claim 33;

(b) isolating a nucleic acid from the environmental sample or treating the environmental sample such that nucleic acid in the sample is accessible for hybridization to the amplification primer pair; and,

(c) combining the nucleic acid of step (b) with the amplification primer pair of step (a) and amplifying nucleic acid from the environmental sample, thereby isolating or

recovering a nucleic acid encoding a polypeptide with a xylanase activity from an environmental sample.

127. The method of claim 126, wherein each member of the amplification
5 primer sequence pair comprises an oligonucleotide comprising at least about 10 to 50
consecutive bases of a sequence as set forth in SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5,
SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID
NO:17, SEQ ID NO:19, SEQ ID NO:21, SEQ ID NO:23, SEQ ID NO:25, SEQ ID NO:27,
SEQ ID NO:29, SEQ ID NO:31, SEQ ID NO:33, SEQ ID NO:35, SEQ ID NO:37, SEQ ID
10 NO:39, SEQ ID NO:41, SEQ ID NO:43, SEQ ID NO:45, SEQ ID NO:47, SEQ ID NO:49,
SEQ ID NO:51, SEQ ID NO:53, SEQ ID NO:55, SEQ ID NO:57, SEQ ID NO:59, SEQ ID
NO:61, SEQ ID NO:63, SEQ ID NO:65, SEQ ID NO:67, SEQ ID NO:69, SEQ ID NO:71,
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NO:83, SEQ ID NO:85, SEQ ID NO:87, SEQ ID NO:89, SEQ ID NO:91, SEQ ID NO:93,
15 SEQ ID NO:95, SEQ ID NO:97, SEQ ID NO:99, SEQ ID NO:101, SEQ ID NO:103, SEQ ID
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NO:115, SEQ ID NO:117, SEQ ID NO:119, SEQ ID NO:121, SEQ ID NO:123, SEQ ID
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NO:215, SEQ ID NO:217, SEQ ID NO:219, SEQ ID NO:221, SEQ ID NO:223, SEQ ID
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30 NO:245, SEQ ID NO:247, SEQ ID NO:249, SEQ ID NO:251, SEQ ID NO:253, SEQ ID
NO:255, SEQ ID NO:257, SEQ ID NO:259, SEQ ID NO:261, SEQ ID NO:263, SEQ ID
NO:265, SEQ ID NO:267, SEQ ID NO:269, SEQ ID NO:271, SEQ ID NO:273, SEQ ID
NO:275, SEQ ID NO:277, SEQ ID NO:279, SEQ ID NO:281, SEQ ID NO:283, SEQ ID
NO:285, SEQ ID NO:287, SEQ ID NO:289, SEQ ID NO:291, SEQ ID NO:293, SEQ ID

NO:295, SEQ ID NO:297, SEQ ID NO:299, SEQ ID NO:301, SEQ ID NO:303, SEQ ID NO:305, SEQ ID NO:307, SEQ ID NO:309, SEQ ID NO:311, SEQ ID NO:313, SEQ ID NO:315, SEQ ID NO:317, SEQ ID NO:319, SEQ ID NO:321, SEQ ID NO:323, SEQ ID NO:325, SEQ ID NO:327, SEQ ID NO:329, SEQ ID NO:331, SEQ ID NO:333, SEQ ID NO:335, SEQ ID NO:337, SEQ ID NO:339, SEQ ID NO:341, SEQ ID NO:343, SEQ ID NO:345, SEQ ID NO:347, SEQ ID NO:349, SEQ ID NO:351, SEQ ID NO:353, SEQ ID NO:355, SEQ ID NO:357, SEQ ID NO:359, SEQ ID NO:361, SEQ ID NO:363, SEQ ID NO:365, SEQ ID NO:367, SEQ ID NO:369, SEQ ID NO:371, SEQ ID NO:373, SEQ ID NO:375, SEQ ID NO:377 or SEQ ID NO:379, or a subsequence thereof.

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128. A method for isolating or recovering a nucleic acid encoding a polypeptide with a xylanase activity from an environmental sample comprising the steps of:

(a) providing a polynucleotide probe comprising a sequence as set forth in claim 1 or claim 24, or a subsequence thereof;

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(b) isolating a nucleic acid from the environmental sample or treating the environmental sample such that nucleic acid in the sample is accessible for hybridization to a polynucleotide probe of step (a);

(c) combining the isolated nucleic acid or the treated environmental sample of step (b) with the polynucleotide probe of step (a); and

20

(d) isolating a nucleic acid that specifically hybridizes with the polynucleotide probe of step (a), thereby isolating or recovering a nucleic acid encoding a polypeptide with a xylanase activity from an environmental sample.

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129. The method of claim 127 or claim 128, wherein the environmental sample comprises a water sample, a liquid sample, a soil sample, an air sample or a biological sample.

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130. The method of claim 129, wherein the biological sample is derived from a bacterial cell, a protozoan cell, an insect cell, a yeast cell, a plant cell, a fungal cell or a mammalian cell.

131. A method of generating a variant of a nucleic acid encoding a polypeptide with a xylanase activity comprising the steps of:

(a) providing a template nucleic acid comprising a sequence as set forth in claim 1 or claim 24; and

(b) modifying, deleting or adding one or more nucleotides in the template sequence, or a combination thereof, to generate a variant of the template nucleic acid.

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132. The method of claim 131, further comprising expressing the variant nucleic acid to generate a variant xylanase polypeptide.

133. The method of claim 131, wherein the modifications, additions or deletions are introduced by a method comprising error-prone PCR, shuffling, oligonucleotide-directed mutagenesis, assembly PCR, sexual PCR mutagenesis, *in vivo* mutagenesis, cassette mutagenesis, recursive ensemble mutagenesis, exponential ensemble mutagenesis, site-specific mutagenesis, gene reassembly, gene site saturated mutagenesis (GSSM™), synthetic ligation reassembly (SLR) and a combination thereof.

15

134. The method of claim 131, wherein the modifications, additions or deletions are introduced by a method comprising recombination, recursive sequence recombination, phosphothioate-modified DNA mutagenesis, uracil-containing template mutagenesis, gapped duplex mutagenesis, point mismatch repair mutagenesis, repair-deficient host strain mutagenesis, chemical mutagenesis, radiogenic mutagenesis, deletion mutagenesis, restriction-selection mutagenesis, restriction-purification mutagenesis, artificial gene synthesis, ensemble mutagenesis, chimeric nucleic acid multimer creation and a combination thereof.

135. The method of claim 131, wherein the method is iteratively repeated until a xylanase having an altered or different activity or an altered or different stability from that of a polypeptide encoded by the template nucleic acid is produced.

136. The method of claim 135, wherein the variant xylanase polypeptide is thermotolerant, and retains some activity after being exposed to an elevated temperature.

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137. The method of claim 135, wherein the variant xylanase polypeptide has increased glycosylation as compared to the xylanase encoded by a template nucleic acid.

138. The method of claim 135, wherein the variant xylanase polypeptide has a xylanase activity under a high temperature, wherein the xylanase encoded by the template nucleic acid is not active under the high temperature.

5 139. The method of claim 131, wherein the method is iteratively repeated until a xylanase coding sequence having an altered codon usage from that of the template nucleic acid is produced.

10 140. The method of claim 131, wherein the method is iteratively repeated until a xylanase gene having higher or lower level of message expression or stability from that of the template nucleic acid is produced.

15 141. A method for modifying codons in a nucleic acid encoding a polypeptide with a xylanase activity to increase its expression in a host cell, the method comprising the following steps:

(a) providing a nucleic acid encoding a polypeptide with a xylanase activity comprising a sequence as set forth in claim 1 or claim 24; and,

20 (b) identifying a non-preferred or a less preferred codon in the nucleic acid of step (a) and replacing it with a preferred or neutrally used codon encoding the same amino acid as the replaced codon, wherein a preferred codon is a codon over-represented in coding sequences in genes in the host cell and a non-preferred or less preferred codon is a codon under-represented in coding sequences in genes in the host cell, thereby modifying the nucleic acid to increase its expression in a host cell.

25 142. A method for modifying codons in a nucleic acid encoding a xylanase polypeptide, the method comprising the following steps:

(a) providing a nucleic acid encoding a polypeptide with a xylanase activity comprising a sequence as set forth in claim 1 or claim 24; and,

30 (b) identifying a codon in the nucleic acid of step (a) and replacing it with a different codon encoding the same amino acid as the replaced codon, thereby modifying codons in a nucleic acid encoding a xylanase.

143. A method for modifying codons in a nucleic acid encoding a xylanase polypeptide to increase its expression in a host cell, the method comprising the following steps:

(a) providing a nucleic acid encoding a xylanase polypeptide comprising a sequence as set forth in claim 1 or claim 24; and,

(b) identifying a non-preferred or a less preferred codon in the nucleic acid of step (a) and replacing it with a preferred or neutrally used codon encoding the same amino acid as the replaced codon, wherein a preferred codon is a codon over-represented in coding sequences in genes in the host cell and a non-preferred or less preferred codon is a codon under-represented in coding sequences in genes in the host cell, thereby modifying the nucleic acid to increase its expression in a host cell.

144. A method for modifying a codon in a nucleic acid encoding a polypeptide having a xylanase activity to decrease its expression in a host cell, the method comprising the following steps:

(a) providing a nucleic acid encoding a xylanase polypeptide comprising a sequence as set forth in claim 1 or claim 24; and

(b) identifying at least one preferred codon in the nucleic acid of step (a) and replacing it with a non-preferred or less preferred codon encoding the same amino acid as the replaced codon, wherein a preferred codon is a codon over-represented in coding sequences in genes in a host cell and a non-preferred or less preferred codon is a codon under-represented in coding sequences in genes in the host cell, thereby modifying the nucleic acid to decrease its expression in a host cell.

145. The method of claim 144, wherein the host cell is a bacterial cell, a fungal cell, an insect cell, a yeast cell, a plant cell or a mammalian cell.

146. A method for producing a library of nucleic acids encoding a plurality of modified xylanase active sites or substrate binding sites, wherein the modified active sites or substrate binding sites are derived from a first nucleic acid comprising a sequence encoding a first active site or a first substrate binding site the method comprising the following steps:

(a) providing a first nucleic acid encoding a first active site or first substrate binding site, wherein the first nucleic acid sequence comprises a sequence that hybridizes

under stringent conditions to a sequence as set forth in SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, SEQ ID NO:23, SEQ ID NO:25, SEQ ID NO:27, SEQ ID NO:29, SEQ ID NO:31, SEQ ID NO:33, SEQ ID NO:35, SEQ ID NO:37, SEQ ID NO:39, SEQ ID NO:41, SEQ ID NO:43, SEQ ID NO:45, SEQ ID NO:47, SEQ ID NO:49, SEQ ID NO:51, SEQ ID NO:53, SEQ ID NO:55, SEQ ID NO:57, SEQ ID NO:59, SEQ ID NO:61, SEQ ID NO:63, SEQ ID NO:65, SEQ ID NO:67, SEQ ID NO:69, SEQ ID NO:71, SEQ ID NO:73, SEQ ID NO:75, SEQ ID NO:77, SEQ ID NO:79, SEQ ID NO:81, SEQ ID NO:83, SEQ ID NO:85, SEQ ID NO:87, SEQ ID NO:89, SEQ ID NO:91, SEQ ID NO:93, SEQ ID NO:95, SEQ ID NO:97, SEQ ID NO:99, SEQ ID NO:101, SEQ ID NO:103, SEQ ID NO:105, SEQ ID NO:107, SEQ ID NO:109, SEQ ID NO:111, SEQ ID NO:113, SEQ ID NO:115, SEQ ID NO:117, SEQ ID NO:119, SEQ ID NO:121, SEQ ID NO:123, SEQ ID NO:125, SEQ ID NO:127, SEQ ID NO:129, SEQ ID NO:131, SEQ ID NO:133, SEQ ID NO:135, SEQ ID NO:137, SEQ ID NO:139, SEQ ID NO:141, SEQ ID NO:143, SEQ ID NO:145, SEQ ID NO:147, SEQ ID NO:149, SEQ ID NO:151, SEQ ID NO:153, SEQ ID NO:155, SEQ ID NO:157, SEQ ID NO:159, SEQ ID NO:161, SEQ ID NO:163, SEQ ID NO:165, SEQ ID NO:167, SEQ ID NO:169, SEQ ID NO:171, SEQ ID NO:173, SEQ ID NO:175, SEQ ID NO:177, SEQ ID NO:179, SEQ ID NO:181, SEQ ID NO:183, SEQ ID NO:185, SEQ ID NO:187, SEQ ID NO:189, SEQ ID NO:191, SEQ ID NO:193, SEQ ID NO:195, SEQ ID NO:197, SEQ ID NO:199, SEQ ID NO:201, SEQ ID NO:203, SEQ ID NO:205, SEQ ID NO:207, SEQ ID NO:209, SEQ ID NO:211, SEQ ID NO:213, SEQ ID NO:215, SEQ ID NO:217, SEQ ID NO:219, SEQ ID NO:221, SEQ ID NO:223, SEQ ID NO:225, SEQ ID NO:227, SEQ ID NO:229, SEQ ID NO:231, SEQ ID NO:233, SEQ ID NO:235, SEQ ID NO:237, SEQ ID NO:239, SEQ ID NO:241, SEQ ID NO:243, SEQ ID NO:245, SEQ ID NO:247, SEQ ID NO:249, SEQ ID NO:251, SEQ ID NO:253, SEQ ID NO:255, SEQ ID NO:257, SEQ ID NO:259, SEQ ID NO:261, SEQ ID NO:263, SEQ ID NO:265, SEQ ID NO:267, SEQ ID NO:269, SEQ ID NO:271, SEQ ID NO:273, SEQ ID NO:275, SEQ ID NO:277, SEQ ID NO:279, SEQ ID NO:281, SEQ ID NO:283, SEQ ID NO:285, SEQ ID NO:287, SEQ ID NO:289, SEQ ID NO:291, SEQ ID NO:293, SEQ ID NO:295, SEQ ID NO:297, SEQ ID NO:299, SEQ ID NO:301, SEQ ID NO:303, SEQ ID NO:305, SEQ ID NO:307, SEQ ID NO:309, SEQ ID NO:311, SEQ ID NO:313, SEQ ID NO:315, SEQ ID NO:317, SEQ ID NO:319, SEQ ID NO:321, SEQ ID NO:323, SEQ ID NO:325, SEQ ID NO:327, SEQ ID NO:329, SEQ ID NO:331, SEQ ID NO:333, SEQ ID NO:335, SEQ ID NO:337, SEQ ID NO:339, SEQ ID NO:341, SEQ ID NO:343, SEQ ID

NO:345, SEQ ID NO:347, SEQ ID NO:349, SEQ ID NO:351, SEQ ID NO:353, SEQ ID NO:355, SEQ ID NO:357, SEQ ID NO:359, SEQ ID NO:361, SEQ ID NO:363, SEQ ID NO:365, SEQ ID NO:367, SEQ ID NO:369, SEQ ID NO:371, SEQ ID NO:373, SEQ ID NO:375, SEQ ID NO:377 or SEQ ID NO:379, or a subsequence thereof, and the nucleic acid
5 encodes a xylanase active site or a xylanase substrate binding site;

(b) providing a set of mutagenic oligonucleotides that encode naturally-occurring amino acid variants at a plurality of targeted codons in the first nucleic acid; and,

(c) using the set of mutagenic oligonucleotides to generate a set of active site-encoding or substrate binding site-encoding variant nucleic acids encoding a range of amino
10 acid variations at each amino acid codon that was mutagenized, thereby producing a library of nucleic acids encoding a plurality of modified xylanase active sites or substrate binding sites.

147. The method of claim 145, comprising mutagenizing the first nucleic
15 acid of step (a) by a method comprising an optimized directed evolution system, gene site-saturation mutagenesis (GSSM™), or a synthetic ligation reassembly (SLR).

148. The method of claim 145, comprising mutagenizing the first nucleic
acid of step (a) or variants by a method comprising error-prone PCR, shuffling,
20 oligonucleotide-directed mutagenesis, assembly PCR, sexual PCR mutagenesis, in vivo mutagenesis, cassette mutagenesis, recursive ensemble mutagenesis, exponential ensemble mutagenesis, site-specific mutagenesis, gene reassembly, gene site saturated mutagenesis (GSSM™), synthetic ligation reassembly (SLR) and a combination thereof.

149. The method of claim 145, comprising mutagenizing the first nucleic
acid of step (a) or variants by a method comprising recombination, recursive sequence
recombination, phosphothioate-modified DNA mutagenesis, uracil-containing template
mutagenesis, gapped duplex mutagenesis, point mismatch repair mutagenesis, repair-
deficient host strain mutagenesis, chemical mutagenesis, radiogenic mutagenesis, deletion
25 mutagenesis, restriction-selection mutagenesis, restriction-purification mutagenesis, artificial
gene synthesis, ensemble mutagenesis, chimeric nucleic acid multimer creation and a
combination thereof.

150. A method for making a small molecule comprising the following steps:

(a) providing a plurality of biosynthetic enzymes capable of synthesizing or modifying a small molecule, wherein one of the enzymes comprises a xylanase enzyme encoded by a nucleic acid comprising a sequence as set forth in claim 1 or claim 24;

(b) providing a substrate for at least one of the enzymes of step (a); and

(c) reacting the substrate of step (b) with the enzymes under conditions that facilitate a plurality of biocatalytic reactions to generate a small molecule by a series of biocatalytic reactions.

151. A method for modifying a small molecule comprising the following steps:

(a) providing a xylanase enzyme, wherein the enzyme comprises a polypeptide as set forth in claim 64, or a polypeptide encoded by a nucleic acid comprising a nucleic acid sequence as set forth in claim 1 or claim 24;

(b) providing a small molecule; and

(c) reacting the enzyme of step (a) with the small molecule of step (b) under conditions that facilitate an enzymatic reaction catalyzed by the xylanase enzyme, thereby modifying a small molecule by a xylanase enzymatic reaction.

152. The method of claim 151, comprising a plurality of small molecule substrates for the enzyme of step (a), thereby generating a library of modified small molecules produced by at least one enzymatic reaction catalyzed by the xylanase enzyme.

153. The method of claim 151, further comprising a plurality of additional enzymes under conditions that facilitate a plurality of biocatalytic reactions by the enzymes to form a library of modified small molecules produced by the plurality of enzymatic reactions.

154. The method of claim 153, further comprising the step of testing the library to determine if a particular modified small molecule which exhibits a desired activity is present within the library.

155. The method of claim 154, wherein the step of testing the library further comprises the steps of systematically eliminating all but one of the biocatalytic reactions used to produce a portion of the plurality of the modified small molecules within the library by

testing the portion of the modified small molecule for the presence or absence of the particular modified small molecule with a desired activity, and identifying at least one specific biocatalytic reaction that produces the particular modified small molecule of desired activity.

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156. A method for determining a functional fragment of a xylanase enzyme comprising the steps of:

(a) providing a xylanase enzyme, wherein the enzyme comprises a polypeptide as set forth in claim 64, or a polypeptide encoded by a nucleic acid as set forth in claim 1 or claim 24; and

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(b) deleting a plurality of amino acid residues from the sequence of step (a) and testing the remaining subsequence for a xylanase activity, thereby determining a functional fragment of a xylanase enzyme.

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157. The method of claim 156, wherein the xylanase activity is measured by providing a xylanase substrate and detecting a decrease in the amount of the substrate or an increase in the amount of a reaction product.

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158. A method for whole cell engineering of new or modified phenotypes by using real-time metabolic flux analysis, the method comprising the following steps:

(a) making a modified cell by modifying the genetic composition of a cell, wherein the genetic composition is modified by addition to the cell of a nucleic acid comprising a sequence as set forth in claim 1 or claim 24;

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(b) culturing the modified cell to generate a plurality of modified cells;
(c) measuring at least one metabolic parameter of the cell by monitoring the cell culture of step (b) in real time; and,

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(d) analyzing the data of step (c) to determine if the measured parameter differs from a comparable measurement in an unmodified cell under similar conditions, thereby identifying an engineered phenotype in the cell using real-time metabolic flux analysis.

159. The method of claim 158, wherein the genetic composition of the cell is modified by a method comprising deletion of a sequence or modification of a sequence in the cell, or, knocking out the expression of a gene.

160. The method of claim 158, further comprising selecting a cell comprising a newly engineered phenotype.

5 161. The method of claim 160, further comprising culturing the selected cell, thereby generating a new cell strain comprising a newly engineered phenotype.

162. An isolated or recombinant signal sequence consisting of a sequence as set forth in residues 1 to 14, 1 to 15, 1 to 16, 1 to 17, 1 to 18, 1 to 19, 1 to 20, 1 to 21, 1 to 22, 1 to 23, 1 to 24, 1 to 25, 1 to 26, 1 to 27, 1 to 28, 1 to 28, 1 to 30, 1 to 31, 1 to 32, 1 to 33, 1 to 34, 1 to 35, 1 to 36, 1 to 37, 1 to 38, 1 to 40, 1 to 41, 1 to 42, 1 to 43 or 1 to 44, of SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:12, SEQ ID NO:14, SEQ ID NO:16, SEQ ID NO:18, SEQ ID NO:20, SEQ ID NO:22, SEQ ID NO:24, SEQ ID NO:26, SEQ ID NO:28, SEQ ID NO:30, SEQ ID NO:32, SEQ ID NO:34, SEQ ID NO:36, SEQ ID NO:38, SEQ ID NO:40, SEQ ID NO:42, SEQ ID NO:44, SEQ ID NO:46, SEQ ID NO:48, SEQ ID NO:50, SEQ ID NO:52, SEQ ID NO:54, SEQ ID NO:56, SEQ ID NO:58, SEQ ID NO:60, SEQ ID NO:62, SEQ ID NO:64, SEQ ID NO:66, SEQ ID NO:68, SEQ ID NO:70, SEQ ID NO:72, SEQ ID NO:74, SEQ ID NO:76, SEQ ID NO:78, SEQ ID NO:80, SEQ ID NO:82, SEQ ID NO:84, SEQ ID NO:86, SEQ ID NO:88, SEQ ID NO:90, SEQ ID NO:92, SEQ ID NO:94, SEQ ID NO:96, SEQ ID NO:98, SEQ ID NO:100, SEQ ID NO:102, SEQ ID NO:104, SEQ ID NO:106, SEQ ID NO:108, SEQ ID NO:110, SEQ ID NO:112, SEQ ID NO:114, SEQ ID NO:116, SEQ ID NO:118, SEQ ID NO:120, SEQ ID NO:122, SEQ ID NO:124, SEQ ID NO:126, SEQ ID NO:128, SEQ ID NO:130, SEQ ID NO:132; SEQ ID NO:134; SEQ ID NO:136; SEQ ID NO:138; SEQ ID NO:140; SEQ ID NO:142; SEQ ID NO:144; NO:146, SEQ ID NO:148, SEQ ID NO:150, SEQ ID NO:152, SEQ ID NO:154, SEQ ID NO:156, SEQ ID NO:158, SEQ ID NO:160, SEQ ID NO:162, SEQ ID NO:164, SEQ ID NO:166, SEQ ID NO:168, SEQ ID NO:170, SEQ ID NO:172, SEQ ID NO:174, SEQ ID NO:176, SEQ ID NO:178, SEQ ID NO:180, SEQ ID NO:182, SEQ ID NO:184, SEQ ID NO:186, SEQ ID NO:188, SEQ ID NO:190, SEQ ID NO:192, SEQ ID NO:194, SEQ ID NO:196, SEQ ID NO:198, SEQ ID NO:200, SEQ ID NO:202, SEQ ID NO:204, SEQ ID NO:206, SEQ ID NO:208, SEQ ID NO:210, SEQ ID NO:212, SEQ ID NO:214, SEQ ID NO:216, SEQ ID NO:218, SEQ ID NO:220, SEQ ID NO:222, SEQ ID NO:224, SEQ ID NO:226, SEQ ID NO:228, SEQ ID NO:230, SEQ ID NO:232, SEQ ID NO:234, SEQ ID NO:236, SEQ ID NO:238, SEQ ID NO:240, SEQ ID

NO:242, SEQ ID NO:244, SEQ ID NO:246, SEQ ID NO:248, SEQ ID NO:250, SEQ ID NO:252, SEQ ID NO:254, SEQ ID NO:256, SEQ ID NO:258, SEQ ID NO:260, SEQ ID NO:262, SEQ ID NO:264, SEQ ID NO:266, SEQ ID NO:268, SEQ ID NO:270, SEQ ID NO:272, SEQ ID NO:274, SEQ ID NO:276, SEQ ID NO:278, SEQ ID NO:280, SEQ ID NO:282, SEQ ID NO:284, SEQ ID NO:286, SEQ ID NO:288, SEQ ID NO:290, SEQ ID NO:292, SEQ ID NO:294, SEQ ID NO:296, SEQ ID NO:298, SEQ ID NO:300, SEQ ID NO:302, SEQ ID NO:304, SEQ ID NO:306, SEQ ID NO:308, SEQ ID NO:310, SEQ ID NO:312, SEQ ID NO:314, SEQ ID NO:316, SEQ ID NO:318, SEQ ID NO:320, SEQ ID NO:322, SEQ ID NO:324, SEQ ID NO:326, SEQ ID NO:328, SEQ ID NO:330, SEQ ID NO:332, SEQ ID NO:334, SEQ ID NO:336, SEQ ID NO:338, SEQ ID NO:340, SEQ ID NO:342, SEQ ID NO:344, SEQ ID NO:346, SEQ ID NO:348, SEQ ID NO:350, SEQ ID NO:352, SEQ ID NO:354, SEQ ID NO:356, SEQ ID NO:358, SEQ ID NO:360, SEQ ID NO:362, SEQ ID NO:364, SEQ ID NO:366, SEQ ID NO:368, SEQ ID NO:370, SEQ ID NO:372, SEQ ID NO:374, SEQ ID NO:376, SEQ ID NO:378 or SEQ ID NO:380; or, consisting of a sequence as set forth in Table 4.

163. A chimeric polypeptide comprising at least a first domain comprising signal peptide (SP) having a sequence as set forth in claim 162, and at least a second domain comprising a heterologous polypeptide or peptide, wherein the heterologous polypeptide or peptide is not naturally associated with the signal peptide (SP).

164. The chimeric polypeptide of claim 163, wherein the heterologous polypeptide or peptide is not a xylanase.

165. The chimeric polypeptide of claim 163, wherein the heterologous polypeptide or peptide is amino terminal to, carboxy terminal to or on both ends of the signal peptide (SP) or a xylanase catalytic domain (CD).

166. An isolated or recombinant nucleic acid encoding a chimeric polypeptide, wherein the chimeric polypeptide comprises at least a first domain comprising signal peptide (SP) having a sequence as set forth in claim 162 and at least a second domain comprising a heterologous polypeptide or peptide, wherein the heterologous polypeptide or peptide is not naturally associated with the signal peptide (SP).

167. A method of increasing thermotolerance or thermostability of a xylanase polypeptide, the method comprising glycosylating a xylanase, wherein the polypeptide comprises at least thirty contiguous amino acids of a polypeptide as set forth in claim 60, or a polypeptide encoded by a nucleic acid as set forth in claim 1 or claim 24, thereby increasing the thermotolerance or thermostability of the xylanase.

168. A method for overexpressing a recombinant xylanase in a cell comprising expressing a vector comprising a nucleic acid sequence as set forth in claim 1 or claim 24, wherein overexpression is effected by use of a high activity promoter, a dicistronic vector or by gene amplification of the vector.

169. A method of making a transgenic plant comprising the following steps:
(a) introducing a heterologous nucleic acid sequence into the cell, wherein the heterologous nucleic sequence comprises a sequence as set forth in claim 1 or claim 24, thereby producing a transformed plant cell;
(b) producing a transgenic plant from the transformed cell.

170. The method as set forth in claim 169, wherein the step (a) further comprises introducing the heterologous nucleic acid sequence by electroporation or microinjection of plant cell protoplasts.

171. The method as set forth in claim 169, wherein the step (a) comprises introducing the heterologous nucleic acid sequence directly to plant tissue by DNA particle bombardment or by using an *Agrobacterium tumefaciens* host.

172. A method of expressing a heterologous nucleic acid sequence in a plant cell comprising the following steps:

(a) transforming the plant cell with a heterologous nucleic acid sequence operably linked to a promoter, wherein the heterologous nucleic sequence comprises a sequence as set forth in claim 1 or claim 24;
(b) growing the plant under conditions wherein the heterologous nucleic acids sequence is expressed in the plant cell.

173. A method for hydrolyzing, breaking up or disrupting a xylan-comprising composition comprising the following steps:

(a) providing a polypeptide having a xylanase activity as set forth in claim 64, or a polypeptide encoded by a nucleic acid as set forth in claim 1 or claim 24;

5 (b) providing a composition comprising a xylan; and

(c) contacting the polypeptide of step (a) with the composition of step (b) under conditions wherein the xylanase hydrolyzes, breaks up or disrupts the xylan-comprising composition.

10 174. The method as set forth in claim 173, wherein the composition comprises a plant cell, a bacterial cell, a yeast cell, an insect cell, or an animal cell.

175. A dough or a bread product comprising a polypeptide as set forth in claim 64.

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176. A method of dough conditioning comprising contacting a dough or a bread product with at least one polypeptide as set forth in claim 64 under conditions sufficient for conditioning the dough.

20 177. A beverage comprising a polypeptide as set forth in claim 64.

178. A method of beverage production comprising administration of at least one polypeptide as set forth in claim 64 to a beverage or a beverage precursor under conditions sufficient for decreasing the viscosity of the beverage.

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179. The method of claim 178, wherein the beverage or beverage precursor is a wort or a beer.

180. A food, a feed or a nutritional supplement comprising a polypeptide as set forth in claim 64.

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181. A method for utilizing a xylanase as a nutritional supplement in an animal diet, the method comprising:

preparing a nutritional supplement containing a xylanase enzyme comprising at least thirty contiguous amino acids of a polypeptide as set forth in claim 64; and administering the nutritional supplement to an animal to increase utilization of a xylan contained in a feed or a food ingested by the animal.

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182. The method of claim 181, wherein the animal is a human.

183. The method of claim 181, wherein the animal is a human.

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184. The method of claim 181, wherein the animal is a ruminant or a monogastric animal.

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185. The method of claim 181, wherein the xylanase enzyme is prepared by expression of a polynucleotide encoding the xylanase in an organism selected from the group consisting of a bacterium, a yeast, a plant, an insect, a fungus and an animal.

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186. The method of claim 185, wherein the organism is selected from the group consisting of an *S. pombe*, *S. cerevisiae*, *Pichia pastoris*, *Pseudomonas* sp., *E. coli*, *Streptomyces* sp., *Bacillus* sp. and *Lactobacillus* sp.

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187. An edible enzyme delivery matrix comprising a thermostable recombinant xylanase enzyme.

188. The edible enzyme delivery matrix of claim 187 comprising a polypeptide as set forth in claim 64.

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189. A method for delivering a xylanase supplement to an animal, the method comprising:
preparing an edible enzyme delivery matrix in the form of pellets comprising a granulate edible carrier and a thermostable recombinant xylanase enzyme, wherein the pellets readily disperse the xylanase enzyme contained therein into aqueous media, and administering the edible enzyme delivery matrix to the animal.

190. The method of claim 189, wherein the recombinant xylanase enzyme comprises a polypeptide as set forth in claim 64.

191. The method of claim 189, wherein the granulate edible carrier comprises a carrier selected from the group consisting of a grain germ, a grain germ that is spent of oil, a hay, an alfalfa, a timothy, a soy hull, a sunflower seed meal and a wheat midd.

192. The method of claim 189, wherein the edible carrier comprises grain germ that is spent of oil.

193. The method of claim 189, wherein the xylanase enzyme is glycosylated to provide thermostability at pelletizing conditions.

194. The method of claim 189, wherein the delivery matrix is formed by pelletizing a mixture comprising a grain germ and a xylanase.

195. The method of claim 189, wherein the pelletizing conditions include application of steam.

196. The method of claim 189, wherein the pelletizing conditions comprise application of a temperature in excess of about 80°C for about 5 minutes and the enzyme retains a specific activity of at least 350 to about 900 units per milligram of enzyme.

197. An isolated or recombinant nucleic acid comprising a sequence encoding a polypeptide having a xylanase activity and a signal sequence, wherein the nucleic acid comprises a sequence as set forth in claim 1.

198. The isolated or recombinant nucleic acid of claim 197, wherein the signal sequence is derived from another xylanase or a non-xylanase enzyme.

199. An isolated or recombinant nucleic acid comprising a sequence encoding a polypeptide having a xylanase activity, wherein the sequence does not contain a signal sequence and the nucleic acid comprises a sequence as set forth in claim 1.

200. An isolated or recombinant nucleic acid comprising a sequence as set forth in SEQ ID NO: 189, wherein SEQ ID NO: 189 contains one or more of the following mutations: the nucleotides at positions 22 to 24 are TTC, the nucleotides at positions 31 to 33 are CAC, the nucleotides at positions 34 to 36 are TTG, the nucleotides at positions 49 to 51 are ATA, the nucleotides at positions 31 to 33 are CAT, the nucleotides at positions 67 to 69 are ACG, the nucleotides at positions 178 to 180 are CAC, the nucleotides at positions 190 to 192 are TGT, the nucleotides at positions 190 to 192 are GTA, the nucleotides at positions 190 to 192 are GTT, the nucleotides at positions 193 to 195 are GTG, the nucleotides at positions 202 to 204 are GCT, the nucleotides at positions 235 to 237 are CCA, or the nucleotides at positions 235 to 237 are CCC.

201. A method for making a nucleic acid comprising a sequence as set forth in claim 200, wherein the mutations in SEQ ID NO: 189 are obtained by gene site saturated mutagenesis (GSSM™).

202. An isolated or recombinant polypeptide comprising an amino acid sequence comprising SEQ ID NO: 190, wherein SEQ ID NO: 190 contains one or more of the following mutations: the aspartic acid at amino acid position 8 is phenylalanine, the glutamine at amino acid position 11 is histidine, the asparagine at amino acid position 12 is leucine, the glycine at amino acid position 17 is isoleucine, the threonine at amino acid position 23 is threonine encoded by a codon other than the wild type codon, the glycine at amino acid position 60 is histidine, the proline at amino acid position 64 is cysteine, the proline at amino acid position 64 is valine, the serine at amino acid position 65 is valine, the glycine at amino acid position 68 is isoleucine, the glycine at amino acid position 68 is alanine, or the valine at amino acid position 79 is proline.

203. A method for reducing lignin in a wood or wood product comprising contacting the wood or wood product with a polypeptide as set forth in claim 64.

204. A detergent composition comprising a polypeptide as set forth in claim 64.

205. A pharmaceutical composition comprising a polypeptide as set forth in claim 64.

206. A method for eliminating or protecting animals from a microorganism comprising a xylan comprising administering a polypeptide as set forth in claim 64.

207. The method of claim 206, wherein the microorganism is a bacterium.

208. The method of claim 205, wherein the bacterium is a salmonellae.

209. An isolated or recombinant nucleic acid comprising SEQ ID NO:189, wherein SEQ ID NO:189 comprises one or more or all of the following sequence variations: the nucleotides at positions 22 to 24 are TTC, the nucleotides at positions 22 to 24 are TTT, the nucleotides at positions 31 to 33 are CAC, the nucleotides at positions 31 to 33 are CAT, the nucleotides at positions 34 to 36 are TTG, the nucleotides at positions 34 to 36 are TTA, the nucleotides at positions 34 to 36 are CTC, the nucleotides at positions 34 to 36 are CTT, the nucleotides at positions 34 to 36 are CTA, the nucleotides at positions 34 to 36 are CTG, the nucleotides at positions 49 to 51 are ATA, the nucleotides at positions 49 to 51 are ATT, the nucleotides at positions 49 to 51 are ATC, the nucleotides at positions 178 to 180 are CAC, the nucleotides at positions 178 to 180 are CAT, the nucleotides at positions 190 to 192 are TGT, the nucleotides at positions 190 to 192 are TGC, the nucleotides at positions 190 to 192 are GTA, the nucleotides at positions 190 to 192 are GTT, the nucleotides at positions 190 to 192 are GTC, the nucleotides at positions 190 to 192 are GTG, the nucleotides at positions 193 to 195 are GTG, the nucleotides at positions 193 to 195 are GTC, the nucleotides at positions 193 to 195 are GTA, the nucleotides at positions 193 to 195 are GTT, the nucleotides at positions 202 to 204 are ATA, the nucleotides at positions 202 to 204 are ATT, the nucleotides at positions 202 to 204 are ATC, the nucleotides at positions 202 to 204 are GCT, the nucleotides at positions 202 to 204 are GCG, the nucleotides at positions 202 to 204 are GCC, the nucleotides at positions 202 to 204 are GCA, the nucleotides at positions 235 to 237 are CCA, the nucleotides at positions 235 to 237 are CCC, or the nucleotides at positions 235 to 237 are CCG.

210. An isolated or recombinant polypeptide comprising an amino acid sequence comprising SEQ ID NO:190, wherein SEQ ID NO:190 comprises one or more or all of the following sequence variations: the aspartic acid at amino acid position 8 is phenylalanine, the glutamine at amino acid position 11 is histidine, the asparagine at amino

acid position 12 is leucine, the glycine at amino acid position 17 is isoleucine, the threonine at amino acid position 23 is threonine encoded by a codon other than the wild type codon, the glycine at amino acid position 60 is histidine, the proline at amino acid position 64 is cysteine, the proline at amino acid position 64 is valine, the serine at amino acid position 65 is valine, the glycine at amino acid position 68 is isoleucine, the glycine at amino acid position 68 is alanine, or the serine at amino acid position 79 is proline.

211. An isolated or recombinant nucleic acid comprising SEQ ID NO: 189, wherein SEQ ID NO:189 comprises one or more or all sequence variations set forth in Table 1 or Table 2.

212. An isolated or recombinant polypeptide encoded by the nucleic acid of claim 211.

213. An isolated or recombinant nucleic acid comprising SEQ ID NO:379, wherein SEQ ID NO:379 comprises one or more or all of the following sequence variations: the nucleotides at positions 22 to 24 are TTC, the nucleotides at positions 31 to 33 are CAC, the nucleotides at positions 49 to 51 are ATA, the nucleotides at positions 178 to 180 are CAC, the nucleotides at positions 193 to 195 are GTG, the nucleotides at positions 202 to 204 are GCT.

214. An isolated or recombinant polypeptide comprising SEQ ID NO:380, wherein SEQ ID NO:380 comprises one or more or all of the following sequence variations: D8F, Q11H, G17I, G60H, S65V and/or G68A.

215. The isolated or recombinant polypeptide of claim 210 or claim 214, wherein the polypeptide has a thermostable xylanase activity.